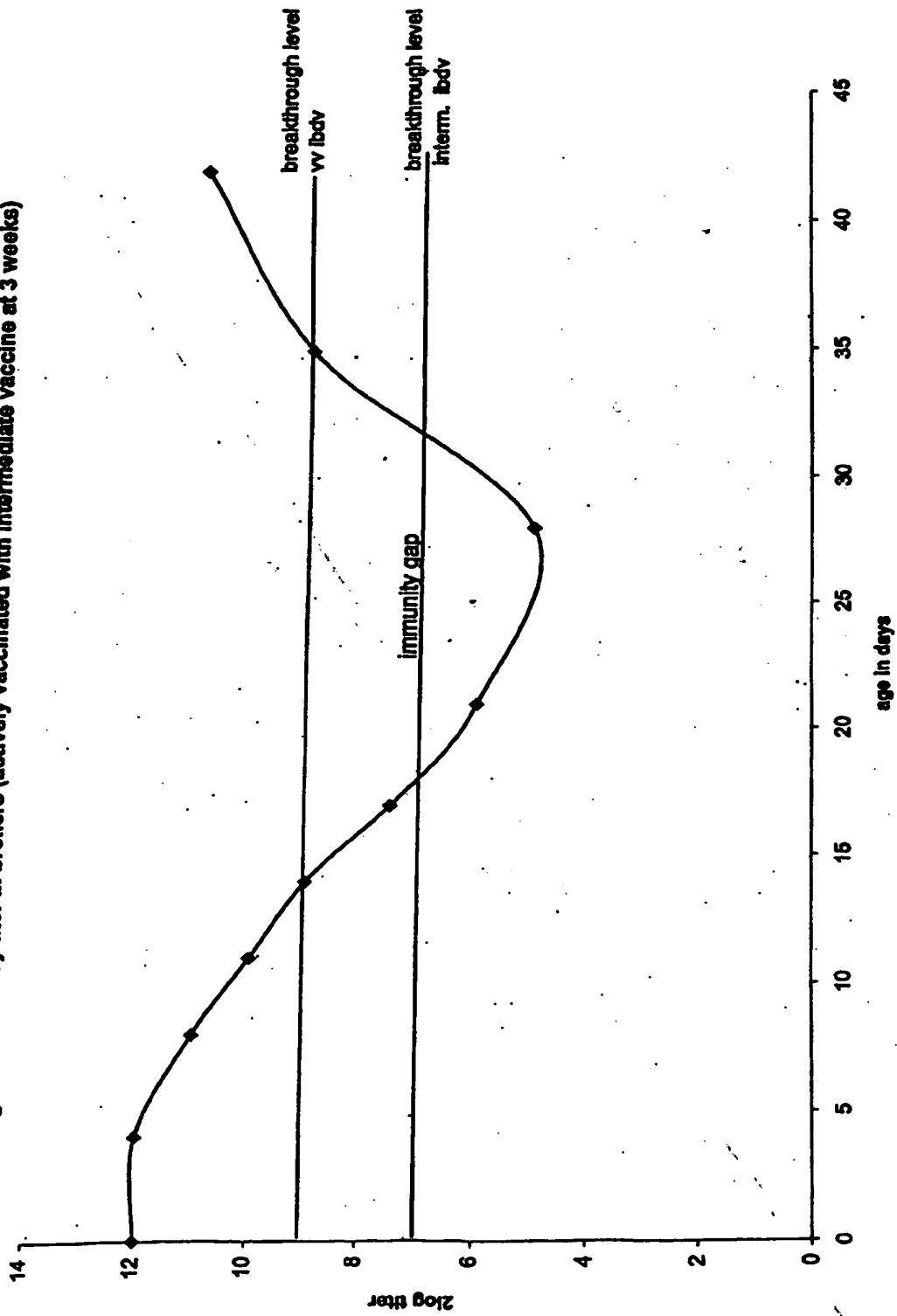


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Figure 1: antibody titer in broilers (actively vaccinated with intermediate vaccine at 3 weeks)



TITLE: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINES

Inventor: Boot et al.
Serial No.: 10/046,671
Docket No.: 2183-5238US

10046671.050602

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Fig.2a Alignment of IBDV A-segment cDNA sequences

Consensus	GGATGAGTC GGTCTGACCC GGGGGGATC ACCCGGGGAC AGGCTGACAA GGTCTGTGTC CAGGTGAGAA CTGCT	75
CEP94-AC.T... ..T.....	75
D6948-AT.A... ..C.....	75
TY89-A	
Consensus	CCTCTACAA TGTATCATTT GATGTTTATG AGGATACAGA CAACGATGTC CAGGCTGAC BACCTGACAA GATCA	150
CEP94-AC..... ..C..... ..A.....	150
D6948-AT..... ..T..... ..G.....	150
TY89-A	
Consensus	AACGACACG ATTGTTCCTT TCATACGAGG CCTCTGTATG CCACACACCG GACCGGGGTC CATTCGGGAC GACAC	225
CEP94-A	225
D6948-A	225
TY89-A	
Consensus	CCTTGGAGG CACACTCTCA GGTCTGAGAC CTCGACCTAC AATTGACTG TGGGGGACAC AGGCTGAGG CTAAAT	300
CEP94-A	...G.....	300
D6948-A	...A.....	300
TY89-A	
Consensus	TGTCTTTTC CTTGGTTTCC CTGCTCAAT TGTGGGTGCT CACTACACAC TGCAGAGCAA TGGGACTAC AAGTT	375
CEP94-AA.....	375
D6948-AT.....	375
TY89-A	
Consensus	CGATCAGTG CTGCTGACTG CCAGAACCT ACCCGGCAAT TACACTACT GCAGGCTAGT GATCGGAT CTGAC	450
CEP94-AT.....	450
D6948-AC.....	450
TY89-A	
Consensus	AGTGAAGTCA AGCAGCTTC CTGGTGGCTT TATGACATA AATGGACCA TAAAGGGCTT GAGCTGCAA GGAAG	525
CEP94-AT..... ..C.....	525
D6948-AC..... ..T.....	525
TY89-A	
Consensus	CCTGATGAA CTGACGATG TTAGCTACAA TGGGTTGATG TCTGCAACG CCAACATCAA GGCAGAAATY GGGAA	600
CEP94-A	600
D6948-A	600
TY89-A	
Consensus	GGTCTGATA GGGGAGGGG TTAGGCTCTT CAGCTTACCC ACATCATAG ATCTTGAGTA TGTGAGCTY GGTGA	675
CEP94-AC..... ..G..T.....	675
D6948-AA..... ..A..C.....	675
TY89-A	
Consensus	GGCATTCGC GGTATGGGC TTGACCCAAA AATGGTAGCH ACATGTGACA GCGTGACAG GCGGAGATC TACAC	750
CEP94-AA..... ..T..... ..C.....	750
D6948-AT..... ..C..... ..A.....	750
TY89-A	
Consensus	CATACTUCA GCGATGATTT ACCAATCTTC ATCAGCTGAC CAACGAGTG GGTGACAT CACTCTTTC TCAGC	825
CEP94-A	825
D6948-A	825
TY89-A	
Consensus	TAATATGAT GGCATACAA GCTCAGCTT YGGGGAGAG CTGTTTTC AAACAGGCTT CCAGGCTT RTACT	900
CEP94-A	C..C..T... ..G..T... ..G.....	900
D6948-A	T..T..C... ..A..C... ..A.....	900
TY89-A	
Consensus	GGGTCTACC ATCTACTTA TAGGCTTGA TGGGACGCG GZAATACCA GAGCTGTGC CCACACAT GGGCT	975
CEP94-A	...C..C... ..C..... ..A.....	975
D6948-A	...T..T... ..T..... ..T.....	975
TY89-A	

TITLE: MOSAIC INFECTIOUS BURSAL DISEASE VIRUS VACCINES

Inventor: Boot et al.
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Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

Fig. 2a Contd.										Alignment of 120V A-Degenerate	Consensus	1050
Consensus	RAGRCGCGC	ACTGACACCC	TTTGGCAAT	CAATTTGTG	ATTCACACA	RCAGAGTAC	CCAGCCATTC	ACATC			1050	
CEP94-A	G...A....	..C.....	..T.....	...C.....A..	A.....	1050	
D6948-A	A...G....	..T.....	..A.....	...A.....C..	G.....	1050	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CATCAACTG	GAGATGTGA	CCTCCAAAG	TGTTGTCAG	GCGGGGATC	AGATGTCAG	GTGCGCAAG	GGGAG			1125	
CEP94-AA.....G..	..G....A	1125	
D6948-AG.....A..	..A....T	1125	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CCTAGCATG	ACGATCCATG	GTGCGACTA	TCAGGGGCC	CTCGGTGCG	TCACCTAGT	AGCATAGAA	AGAT			1200	
CEP94-AT..G.....	G.....	1200	
D6948-AC..A.....	A.....	1200	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	GCGACAGGA	TCGTGTGTA	CGGTGCTGG	GGTGACAC	TTGAGCTGA	TCGCAATCC	TGACTAGCA	AGGA			1275	
CEP94-AC.....T..	1275	
D6948-AT.....C..	1275	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CCTGTTACA	GATGAGGCC	GATTTGCC	AGTAGCCATG	AATACACAA	AATGTACT	GATGTAGAG	GAAG			1350	
CEP94-AT..	1350	
D6948-AC..	1350	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	TCTTGATC	AGAGCCGAT	GCGACACAG	GATGTACT	GACTTGTG	ATGACTTCT	GAGGTGCGC	GAAT			1425	
CEP94-AA..T..	..A.....	1425	
D6948-AC..T..	..G.....	1425	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CACTCTGCC	CTGAGATG	CAAGACAT	TGCTTCAA	GACATATCC	GGGCGTAG	GAGGATGCT	GTGC			1500	
CEP94-A	C.....A.....	1500	
D6948-A	T.....C.....	1500	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	GTTGTTCT	ACATTTTCC	CAGTGGCC	TGCTTAGCC	CATGATTT	GAGAGTGT	AGATGACTG	CTGG			1575	
CEP94-AC..	..T.....	..T.....	1575	
D6948-AT..	..C.....	..C.....	1575	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CAATGAGCA	CAGCTCTTT	CAGGACTGC	TGAGGCCCG	TCAGGAAAG	CAGGACTGC	CTCAGGCCG	ATAG			1650	
CEP94-A	1650	
D6948-A	1650	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	GCACTACT	CTCGGGCG	ACAGGGGTA	GAGGTATC	GCAATCTT	TTGAGTGC	CCAGATCTT	GTGT			1725	
CEP94-AG..A..	..C.....C..	1725	
D6948-AA..G..	..T.....T..	1725	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CGACGGAT	CTTCTTAC	CTGGGTACT	CGGGGTGA	CACAGCTG	ACTGCTTT	AGAGAGGT	GCCAC			1800	
CEP94-AT.....G..T..	A.....	1800	
D6948-AC.....A..C..	G.....	1800	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	GCTATTCCCT	GTGTTATTA	CGACATGGA	AGATGCCATG	ACGCCCAAG	CAATTGACAG	CAAAATTTT	GCTGT			1875	
CEP94-AT..TC.....T.....	1875	
D6948-AC..CT.....C.....	1875	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		
Consensus	CATTTGAGC	GTGCGAGAG	ATCTCCAA	TCGTTCTCA	AGGAGATCT	TCATAGAGC	TCTCTCTGA	CAAG			1950	
CEP94-AC.....	..T.....T..	..C..	1950	
D6948-AT.....	..A.....C..	..T..	1950	
TT89-A	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----		

TITLE: MOSAIC INFECTIOUS BURSAL DISEASE VIRUS VACCINES

Inventor: Boot et al.
Serial No.: 10/046,671
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Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

Consensus	AGTCTATGGA TATCTCTCAG ATGGGTTACT TCCACTGGAG ACTGGGAGAG ATATACACCT KUTCCCAATA GATGA	2023
CEP94-AC..... T.....	2023
D6948-AT..... G.....	2023
TY89-A	
Consensus	TGTCTGGAC GACGACATTA TCTCTCCAA AGATCCCAAT CCTCTATTG TGGGAACAG TGGAAATCTA GGCAT	2100
CEP94-AT.....	2100
D6948-AC.....	2100
TY89-A	
Consensus	AGCTACATG GATGTGTTT CACCCAAAT CCATATCAT GTGGCTATGA CCGGAGCCCT CAATGCTTCT GCGA	2175
CEP94-AA..... ..T.....	2175
D6948-AC..... ..C.....	2175
TY89-A	
Consensus	GATTGAGAA GTAGCTTTA GAGCACCAG CTCGCCACT GCACACGAC TTGGCTTAA GTTGGCTGAT CCGG	2250
CEP94-AA..A.....	2250
D6948-AC..G.....	2250
TY89-A	
Consensus	WCAATTGAT GTTACACCG GTTCCACTG GGCACGCTT ATCAACCTT TTCTTCACAA TCCGCGGAC TGGG	2325
CEP94-A	A....C..T..A..... ..C..... ..A....C.....	2325
D6948-A	T....T..C..G..... ..T..... ..G....T.....	2325
TY89-A	29
Consensus	CAGGTTCCCT TACTCAACC TCCCTATCT TCCACGAGG GCGGACCTC AGTACATCT KCCCTGGCH GCCTC	2400
CEP94-A	...C..C..C..... ..A..A..C.. T....C..AT..A....C.....	2400
D6948-A	...C..C..T..... ..T..A..C.. T....C..AT..A....C.....	2400
TY89-A	...T..A..C..... ..T..C..T.. C....A..CA..T....T.....	104
Consensus	MGATTCAAA GAGACCCCG AACTGAAAT TCTGTGAGG GCAATGAGG CACGACGCA COTGGACCA TYTTP	2475
CEP94-A	A..... ..C..... GAG T..C..CA..A..A....A..A..A..C.....	2475
D6948-A	A..... ..C..... GAG C..C..CA..A..C....A..A..A..C.....	2475
TY89-A	C..... ..A..... AGA C..T..GC..T..A....C.....	179
Consensus	CCCTGCGC CTCTGCTT TCTGTGCTT GAGAGAAAT GCGATGTGA CTGATATGC TACTTGGCH CTCAG	2550
CEP94-A	..AA..T..A...AGT..G..... ..C..... ..G..T.....	2550
D6948-A	..AA..T..G...AGC..G..... ..C..... ..G..T.....	2550
TY89-A	..GC..A..T...CAG..C..... ..T..... ..A..C.....	254
Consensus	CGACCCGAC GGCATGGA TGGGAATTT YCTGCAAT GCGGCGAG CCGGACGCA GTCCARAG GCCAA	2625
CEP94-AC..TC..... ..CGA..... T..T....C..A..A..A..A..C.....	2625
D6948-AC..TC..... ..CGC..... T..C....C..A..A..A..A..C.....	2625
TY89-AA..CA..... ..AAA..... C..A....T..T..C..G..C..A.....	329
Consensus	GTATGGACR GCGGCTACG GATGAGGAC TGGGCCCC ACOCGAGG ARGACAGG GAGAAAGAC ACAG	2700
CEP94-A	...C..G..A..A..... ..TC..G..... ..A....G..A.....	2700
D6948-A	...C..G..A..A..... ..CC..G..... ..T....G..A.....	2700
TY89-A	...T..C..G..T..... ..TA..A..... ..G....A..G.....	404
Consensus	GATCTGAG AGATGAGA CBTATGGAT CTACTTCCA ACACCGAAT GGTAGCACT CAATGGCAC CGGG	2775
CEP94-AA..... ..G..C..... ..T.....	2775
D6948-AA..... ..G..T..... ..T.....	2775
TY89-AC..... ..A..G..... ..C.....	479
Consensus	SCCAAGCCC GCCAGCTTA AGTACTGCA AACACAGG GAAATACCG AHCAGACGA GAGTATCTA GACTA	2850
CEP94-A	G..... ..A..... ..G.....C..... ..C..A.....	2850
D6948-A	G..... ..G..... ..G.....C..... ..T..T..A.....	2850
TY89-A	C..... ..C..... ..A.....A..... ..A..C.....	554
Consensus	TGTCAATG GAGAGAGCC GGTGGGCTC AGAGAGAC RTCTTAAAG CAGTACCTC GATCTAGG GCTCC	2925
CEP94-A	C....T..A..... ..A..... ..A..A..C.....	2925
D6948-A	C....T..A..... ..A..... ..A..A..C.....	2925
TY89-A	T....C..G..... ..G..... ..G..T.....	623

TITLE: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINES

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Serial No.: 10/046,671
Docket No.: 2183-5238US

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Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

Consensus	AGGACAGGCG GAGCCACCCC AACCTTTCAT AGACGAGGT OCCARSTCT ATGAAATCAA CAGTGGGCT GGTCC	3000
CEP94-AA ..G..... ..T..... ..T..... ..AA..... ..A..... ..C.....	3000
D6948-AA ..G..... ..C..... ..C..... ..AA..... ..G..... ..C.....	3000
TY89-AT ..A..... ..C..... ..C..... ..CG..... ..G..... ..T.....	784
Consensus	HAACCAAGAG CAGATGAAG ATCTGCTCTT GACTGGGATG GAGATGAGC ATGCAATCC CAGCGGGCT CTAC	3075
CEP94-A	A.....A..AA. .T.....T.	3075
D6948-A	C.....A..AA. .T.....C.	3075
TY89-A	A.....G..GG. .C.....C.	779
Consensus	AAAGCCGAG CCAAAACCCA ATGCTCCMC ACAGAGACCC CCGGCGGCG TGGGCGGCTG GATCAGGCG GTCTC	3150
CEP94-AC.....A..... ..T..... ..A.C.....	3150
D6948-AC.....A..... ..T..... ..G.T.....	3150
TY89-AA.....T..... ..A..... ..A.G.....	854
Consensus	TGATGAGAC YTGAGTGAG GYNCTGGGA GTCTCCGAC ACCACCCCG CAGGTGTGGA CACCACTTA KMETT	3225
CEP94-A	...T..... C.T..... .TA..... ..T..... ..CG GACT.	3225
D6948-A	...T..... C.T..... .CT..... ..C..... ..CG GACA.	3225
TY89-A	...C..... T.G..... .CT..... ..T..... ..AA TCAC.	929
Consensus	ASMGATTCG AAATTGATC CATTGCGGG TCCCC	3260
CEP94-A	.CAAC..C.C	3260
D6948-A	.CAAC..C.C	3260
TY89-A	.GTGA..T.G	964

TITLE: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINES

Inventor: Boot et al.
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Fig.2b

Alignment of IBV B-segment cDNA sequences

Consensus	GGATACGAGG GGTCTGACCC TCTGGAGTC AGGAATAC GTGGCTACA GGGGATGAT CCGCCCTG CTGC	75
CEP94-BC...AA ..G....G.	75
D6948-BT...GC ..A....A.	75
Consensus	ACGTTATGG CTCTCTCTCT TGTAGTCTT ECGACCATGA GTGACCTTT CAATAGCCA CAGGCGCA GCAG	150
CEP94-BG..... ..A.... ..C..... ..C.	150
D6948-BA..... ..G.... ..T..... ..A.	150
Consensus	ATHTCAGCG GTTCGGCAT AAGGCTACG OCTGACAG ATGTGAGGA ACTCTGATC CCTAAGTTT GGTG	225
CEP94-B	..C..... ..T..... ..A.... ..C..... ..T..... ..A..T.	225
D6948-B	..A..... ..A..... ..G.... ..T..... ..C..... ..G..C.	225
Consensus	CCACCTGAG ATCCTTTC CAGCCTAGT CAGCTGCGA AGTCTCTCG RGAAGCGC TACAAGTTT TCGG	300
CEP94-BGC.T.A....A.A..G.... ..AG..T.	300
D6948-BCT.G.T..... ..G....A.G..A.... ..GA..C.	300
Consensus	CCACGCTTC TACCTGAGA TGAAGATAT GAGCGGATC AATACTCC WGAATGCG TGAATGCG AGTA	375
CEP94-BG..C..... ..C..... ..A...T....AC.A.	375
D6948-BA..T..... ..T..... ..T...C....TA.G.	375
Consensus	GAGGCGCTG TTATAAAC CACTTACT CTCCATATG GAGATCAGA GTACTTCG AAGACTAC CACA	450
CEP94-B	..A..G.... ..C..T..... ..T..... ..T..... ..A..G.... ..A..... ..	450
D6948-B	..G..A.... ..A..C..... ..C..... ..C..... ..T..... ..A..... ..	450
Consensus	CATCGGCGA GCAGGAGAA GCGCATGCG TACCGCGCG ATATGCAAT ACTCAGCG AGTATTAAT TGTG	525
CEP94-B	..T....T.G.... ..C..... ..C..... ..T....CC..T.	525
D6948-B	..C....G.A..... ..C....T....TC..T.	525
Consensus	CTCCAGGTC CAGAGGCGA WGAAGCTG AAGATGAG TACCTTCTT TACCGAATC ATWAGGAGA AGCC	600
CEP94-B	..A.....A C..GG...A ..G....A. ..A....CT. G..... ..A..G..C. ..G...	600
D6948-BC.....C A..TAA..T ..A....G. ..C....AC. A..... ..T..A..T. ..A...	600
Consensus	TATGAGTGG GACCTACAT GAGACAGCG ACTGACTTG TGTATGAA TGGGTTGCC ACTGAGAA ACCA	675
CEP94-B	..T..A.... ..A....A ..TC..... ..G..C.... G....C.... ..A..... ..	675
D6948-B	..C..G.... ..G....C ..CA..... ..T..T.... A....T.... ..G..... ..	675
Consensus	AACAGATTC CTCTAAGCT TGGTACAT TTGAGGCA TGGGAGCT ACTTGATC ACATACCG TAGG	750
CEP94-BG..... ..T..... ..C..G.... ..AC..... ..	750
D6948-BA..... ..C..... ..A..C..... ..TT..... ..	750
Consensus	CCACCGGTC AGGATGAGA GCGCTGCTA CCACTCACA GGTGCGGTC AAGGATGTC GTCTGACG GAGC	825
CEP94-BG..... ..A..... ..C..... ..A..... ..A...	825
D6948-BA..... ..G..... ..A..... ..T..... ..C...	825
Consensus	GTGATGCG AMTTTGGGT TGAGATTC CTCCGAAA TCACTCAG GTCATAGT GACTGCTT ATGT	900
CEP94-BC..C..... ..A..T.... ..	900
D6948-BG..A..... ..G..C.... ..	900
Consensus	GATGACCA AAGGAGAC WATGGSAG ATGATAGTA TTTCAACCA GTTCTTGA GAGCTATC CACT	975
CEP94-BG..A....C.... ..T....C..A.... ..CA..... ..A..A....	975
D6948-BA..T....G.... ..C....A..G.... ..TC..... ..G....G....	975
Consensus	YTGAGCAG GTGAGGAG AAGGCTCA AACAGAGA AGCTCTCG CATGTAGT GACTATGT ACTA	1050
CEP94-B	T.....A.G....AA..... ..T..... ..T..... ..	1050
D6948-B	C.....G.A....GG..... ..C..... ..C..... ..	1050
Consensus	TATGTGCG TTGTGTTCC WAGGCTGAG AGGTACAGA AAGTACAT GCTACCAAG ACCGAGCA TGGG	1125
CEP94-BC.... ..A..... ..G..... ..T..... ..G..... ..	1125
D6948-BT.... ..C..... ..C..... ..C..... ..T..... ..	1125
Consensus	TCACTCAT CCGCAACACA CTTATGATC TGTATGATG CTTGCGGCT GATGTGCAAT ACCGAGAA ACAT	1200
CEP94-BC..... ..T....C.C..... ..T..... ..	1200
D6948-BA..... ..A....A.T..... ..T..... ..C..... ..	1200

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DISEASE VIRUS VACCINESInventor: Boot et al.
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Fig.2b Contd. Alignment of IBDV B-segment cDNA sequences

Consensus	TGAAACATG	ARGGGTGTCC	RTNCCTTAC	AAATTCACCC	CGTTAGAGG	WGGGTTGAC	AGGTCGTGG	AGTGG	1273
CEP94-B	A.....	A.....	..A.....	...C.....	A...T.G...C.....	1273
D6948-BG.....	G.....	..G.....	...T.....	T...C.A...G.....	1273
Consensus	ATATGCTTC	CGGAGAAC	CAAGCTTTW	GTATTTGCG	ACACATATA	CATTGTTAC	TGACACAGT	GGTAC	1330
CEP94-B	...T...C.	...A.....TC.TG.....C.....	..A.....	1330
D6948-B	...A...T.	...T.....CT.AT.....	1330
Consensus	TCAATTGAC	TAGAGAGGG	TGAGGCAAC	TGACACGTC	AACACATCA	AGCCCGGTC	TACTACATC	TGACC	1425
CEP94-BT..C.	A....A...A..C...	1425
D6948-BG..T.	G....C...C..T...	1425
Consensus	AGAGGTGTT	CGATTAACG	TGACCGATG	TTCATCACA	CATGGGCGAC	CTTTCGATG	AACCTGCCC	CGGCT	1500
CEP94-BG....	..A..C....	C.....A...A.....C.....G...	1500
D6948-BA....	..C..T....	T.....C...G.....	1500
Consensus	CTAGTGTGG	ACTCATCTG	TCTGATGAT	AACCTTCAC	TTAGACGTA	TGTCAGGTC	AGTGGGATG	CAGCC	1575
CEP94-BG....G..	C.....A...G..A..	..T....C..C.....	1575
D6948-BT....A..	T.....T...T..G..	..C....A..T.....	1575
Consensus	ACCTTCATC	ACAACCACT	TTTACGACC	CTGTGCTTG	ACCATGCGA	CTTGATGAT	CACCTACGC	CAGAC	1630
CEP94-B	..G.....C..	CT.G....G	..A....T.C.....	GA...G..C..A.	1630
D6948-B	..C.....T..	TC.T....C	..T....A.T.....	AG...A..T..T.	1630
Consensus	AGCAGAGAT	TCAATCAAT	TGAGACAGG	CTGGATATC	ACTTTAAGT	TGAGAGTTC	ATTGATGAT	TGAGG	1725
CEP94-BG....A....A....	..A..T...	...T....T..C...	1725
D6948-BA....G....A....	..G..C...	...C....C..T...	1725
Consensus	GGCAAGCTA	GACAGCTTT	CTCTCTGCA	CAGCAGGAT	ACCTGATGG	AGGGGTTGA	CGAGACAAAT	CGAGC	1800
CEP94-BG.T.....G....T...A..T...	1800
D6948-BC.C.....A....C...G...C...	1800
Consensus	CGAAGTGG	AGCTGACCT	ACTGGGTTG	TGAGGACAT	ACAGCAAGA	TCTTGGGATC	TATGTCGGG	TGCTT	1875
CEP94-BT.	...T....	..A..G...	..A..T..A.C.....	1875
D6948-BA.	...G....	..C..A...	..T..A..T.T.....	1875
Consensus	GACAGGAC	GCTTTTTC	TTCTGCTGG	TATCCCAAG	GGTAGAGAA	TAAGATCTC	AAATCCCAAG	TTGGG	1950
CEP94-BC.....	T.....G..	..A.....	C..G..T...	..G....A..C...	1950
D6948-BT.....	C.....A..	..G.....	T..A..C...	..A....G..T...	1950
Consensus	ATGAGGAG	CATACAGAT	WTCAGTAT	GAGGCGTTG	GTTGATAGG	TGTTGAGAC	TACCCACTCC	TGAC	2025
CEP94-BG.G..	A.....T	2025
D6948-BA.A..	T.....C	2025
Consensus	AAAGCTTCA	AGATTAATC	AGTGTCTCT	CGGCGGATC	TGAGGCGCA	GGGTTTCCG	CTGATGAGT	TGCTT	2100
CEP94-BC....	...T..C..	..G..C..C..A.....C.....A	2100
D6948-BT....	...C..T..	..A..T..A..C	2100
Consensus	GGGAGTGT	CGATGTTTC	AGATGTCGG	GAGCTTTGG	AAAGCTTCA	TATCAGCTG	ACATGACAT	CGGAG	2175
CEP94-BT..C...	A.....T	..G..C...	T.....	..C.....T..T...	2175
D6948-BA..T...	C.....A	..A..T...	C.....	..A....C..G...	2175
Consensus	AGCTTGGCG	AACATACAC	AGAGTACCC	CCCAATCTC	CAATGTCAC	CAGACAGTC	AACATGAGG	GGCTT	2250
CEP94-BA....G....	A.....G..G..C..T..G..A..C	2250
D6948-BC....T..G	A.....TA..T.C..T..G..A	2250
Consensus	AAAGCAGTC	GCAATGCCCT	CAGACCGGT	CGATATAGA	ATGAGCGCG	ACTGATGAT	CTGCTCTCTC	TAGCC	2325
CEP94-BC.....TC..G..G....T	2325
D6948-BT.....CT..A..T.....	..A....CC.....	2325
Consensus	ACGAGGAGA	GGGCTTCA	AGATGAGAT	AAAGCCAGG	CAGAGCGGA	GAACTCCAC	AGCTTACG	CGGAT	2400
CEP94-B	..A..AA..A.	...T..G..	A..T....TA.....C....	..A..C	2400
D6948-B	..C..CC..C.	...A..A..	G..C....CG.....T....	..C..T	2400

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Fig.2b Contd. Alignment of IBDV B-segment cDNA sequences

Consensus	GAACCCGCTG CAGACTGCTT TGAAGTCTCA GAACTCTCTT CAGACTCTCT GAGAAAGCC GACCTTCCCA CCAG	2473
CEP94-B C...A.A... ..T... ..T... ..C.... ..	2475
D6948-B T...C.G... ..C.... ..G... ..F.... ..	2475
Consensus	GTGCTCTACT CAGACTGCTT GGAACAGAC GAGCTCTCTT AAGCTCTTCA GTCTACTTCH GTCTACACTC CCAG	2550
CEP94-BC.... ..C.... ..A..T.. ..G..T..C ..T... ..C....	2550
D6948-BT.... ..T.... ..G..C.. ..A..C..A ..C.... ..A....	2550
Consensus	TACCCAGAG TYAAGAACCC ACGACCCGCC TCCACCCCGG TTCTGGGCT CCACCTGCCC GCCAAGAGG CCAC	2625
CEP94-BA..C..... ..A..... ..A..... ..A..... ..A.....	2625
D6948-BG..T..... ..G..... ..G..... ..G..... ..G.....	2625
Consensus	GGTGTCCAG CAGCTCTTCT CGAGCAGG ACAGCAGAC CAGTGGGCT GAGCTCTCA ACGCTCTCA AGAC	2700
CEP94-BC..... ..A..... ..C..... ..C..... ..C.....	2700
D6948-BA..... ..G..... ..T..... ..T..... ..T.....	2700
Consensus	GGCTGAAA TGGCCAAAG GCGGCAAGC CAAAGAGGA GCGGCAAYA GCGATGTGG GAGCTCTCA AGAG	2775
CEP94-BC..... ..G..... ..C..... ..C..... ..C.....	2775
D6948-BA..... ..A..... ..A..... ..A..... ..A.....	2775
Consensus	AGGACATAA TCCAGAGCC GGTATCCCG GCTTGGGCT GCGGGGGGCC CC	2827
CEP94-BT..... ..T..... ..T..... ..T..... ..T.....	2827
D6948-BC..... ..C..... ..C..... ..C..... ..C.....	2827

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Fig.3a	IBDV polyprotein alignment									
Consensus	NTDLQDTQQ	IVFFILSLM	PTTGFASIPD	DYLEKSTLAS	STSTELATVG	DTGSLIVTF	PGFTOSIVGA	HYELO		75
CEP94-PP		75
D6948-PP		75
TT89-PP		
Consensus	ENGTHTFDQM	LLTAGELPAS	INTCLVENS	LTFRSTTLFG	GVTLNQTIN	AVTPQOSLEN	LTQVSTHLEL	SEMAN		150
CEP94-PP		150
D6948-PP		150
TT89-PP		
Consensus	IRKIGNVLV	GGVTVLSLP	TSYELQVEL	GGPIPAIGLD	PMVATCDSS	DSPKVTITA	ADDTQFESQY	Q.GGV		225
CEP94-PPP..		225
D6948-PPA..		225
TT89-PP		
Consensus	TYTLPSANID	AITELS.GGE	LWPTSEV.GL	.LGATVYLIG	PDGTAVITRA	VAA.SGLT.S	TEEL.PTH.V	IFT.E		300
CEP94-PPV..E..	..V..H...T..	..L...L..	..N..	300
D6948-PPD...A..	..M...I..	..S..	300
TT89-PP		
Consensus	ITQPTISIEL	KIVTRESQQ	AGDQNEEA	GLAVTINOC	HTFGALRPVT	LVATERVATG	SVTVAGVEN	FELIP		375
CEP94-PP		375
D6948-PP		375
TT89-PP		
Consensus	NPFLAQLVY	IKGFDPQGM	HTTELILSR	DALGIKTVWF	TREYTDREY	FMEVAKNSP	LEKMGFQFK	DIIRA		450
CEP94-PP		450
D6948-PP		450
TT89-PP		
Consensus	.KRIAVFVVS	TLPTFAFLA	NAIGSDVYL	LGDEQAASG	TARAAGKAR	AASGRIRQLT	LAADQYEVV	AKLQ		525
CEP94-PP	I.....		525
D6948-PP	L.....		525
TT89-PP		
Consensus	VPQPVVDGI	LASTG.LGA	HELDVLRG	ATLFTVVIT	VEDANTFKAL	NSKQFAVING	VREDLQPPSQ	RGEVI		600
CEP94-PP		600
D6948-PP		600
TT89-PP		
Consensus	RTLGRNVYQ	YAFQVLSLE	TGRTTVVVI	DDVMDSTEL	SGDFIPPIVG	NSGRLAIAYN	DVFRKRVFIN	VAMTG		675
CEP94-PP		675
D6948-PP		675
TT89-PP		
Consensus	ALMA.GKIR.	VSRSTELAT	AMELGLKLG	FGAFVVTG.	NSGTFIKRFP	NSPDRNDEL	YIALPTLPFN	AGRQY		750
CEP94-PP	...C...K		750
D6948-PP	...Y...N		750
TT89-PPT...P		28
Consensus	HLMAASEFK	ETPELEAVR	AMEAANVDP	LPQALSVPN	MLEKNGIVTD	KANVALSDSN	AMNSQVLAN	APQAG		825
CEP94-PP		825
D6948-PP	D.....		825
TT89-PP	...L.....	...D...	...D.....	...R...Q...K.....		103
Consensus	SEKQAKYOT	AGTQVANGP	TYEAGREK	TRISKEMTH	GIYVATPENV	ALSGRNGPSP	QQLKYNQTR	EIFDP		900
CEP94-PP		900
D6948-PP		900
TT89-PPE..		178
Consensus	KEDYLYVHA	EKRLASERQ	ILRANTSTG	APQQAEPQA	FIDEVAKVYE	INSGRQPSQ	QKDLALTAM	ESKIR		975
CEP94-PP		975
D6948-PP		975
TT89-PP	...F.....	V.....R...		253
Consensus	KPRRAPPKK	KPRAPTORP	PGRLGRGRT	VSEKDLK						1012
CEP94-PP	...L.....						1012
D6948-PPA.....						1012
TT89-PPS.....						290

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Fig.3b IBDV VP1 alignment

Consensus	MSD.FEETQA RS.ISAAGFI EPTAGQDVEE LLTPKWWTF EDPLASTPEL AKFLAKENYK .LQFSLFEN EHYET	75
CEP94-VP1	...I..... ..T.....	75
D6948-VP1	...V..... ..K.....	75
Consensus	DQILFDLAMI RQIEGAVLKP TSLFIDGGE YFHCYTFER PSKIKHAYT PDIALLEQKI YLFLQVPEA. ...LKD	150
CEP94-VP1N EG...	150
D6948-VP1T DN...	150
Consensus	EVTLLTQWIR DEATGSGTTH QQATRLVANK EVATGSHPK DFLKLYTPE SIAGLLDITL FVQPPQEDER FAVPL	225
CEP94-VP1	225
D6948-VP1	225
Consensus	TRVPSRLAL TGVVDG.FEV EDYLPKHLK EGGSLTYGR TGTGTIGKI AIDKFLREL S.LLKQAQT EENK	300
CEP94-VP1D..... ..T.....	300
D6948-VP1E..... ..A.....	300
Consensus	KLLSLKLVY WYLSGLLFP KARYDKSTW LKTRQWHA PPTPLHLN ITWFWHSEF NVFLMDECP ELKYP	375
CEP94-VP1	375
D6948-VP1	375
Consensus	KPTGRLAKI VEMI.AP.EP KALVADNIY IVEHWITSI DLEKHAQCT RQHQAMTY ILTRQWDSG DFWN	450
CEP94-VP1L..E..	450
D6948-VP1M..D..	450
Consensus	QTVATYAKI APALVDEEC LIDELQIKTY QQSGHAYT DSHLLSTLV LDQKLM.QP .FQSEFESI ERLG	525
CEP94-VP1E.. E.....	525
D6948-VP1K.. S.....	525
Consensus	DEPKERSID DIRMGLQLV .LAQGYLGG QVEFSQ.SPT VELDLQWHA TIRKILQIV FVLKRELFC SAATP	600
CEP94-VP1L..... ..S.....	600
D6948-VP1F..... ..F.....	600
Consensus	KVVEKELKE KVQIEQAYV VYEAELVVG GASTYLLKHA CQMA.AARR KLEAKOFFLD EFLAKSELS EFGHA	675
CEP94-VP1G.....	675
D6948-VP1S.....	675
Consensus	FETPKIKLV T.EKLAKL. PPTPEPPEVM RIVWTOGLEA VEMALTOY KHEAGLSGLV LLATARSLO DAVIA	750
CEP94-VP1S..... ..K.....	750
D6948-VP1P..... ..E.....	750
Consensus	KAKKILKES KPDDPDADMY ERSETLSLL EKADIASKVA REALVETSDA LEAVQSTSVY TKNTEVEMP QTASH	825
CEP94-VP1	825
D6948-VP1	825
Consensus	FVGLKLPK RATOVQALL GAGTSAPKCH EAPTASINAV KAKKQKQK ESQ..	881
CEP94-VP1QP	881
D6948-VP1--	879

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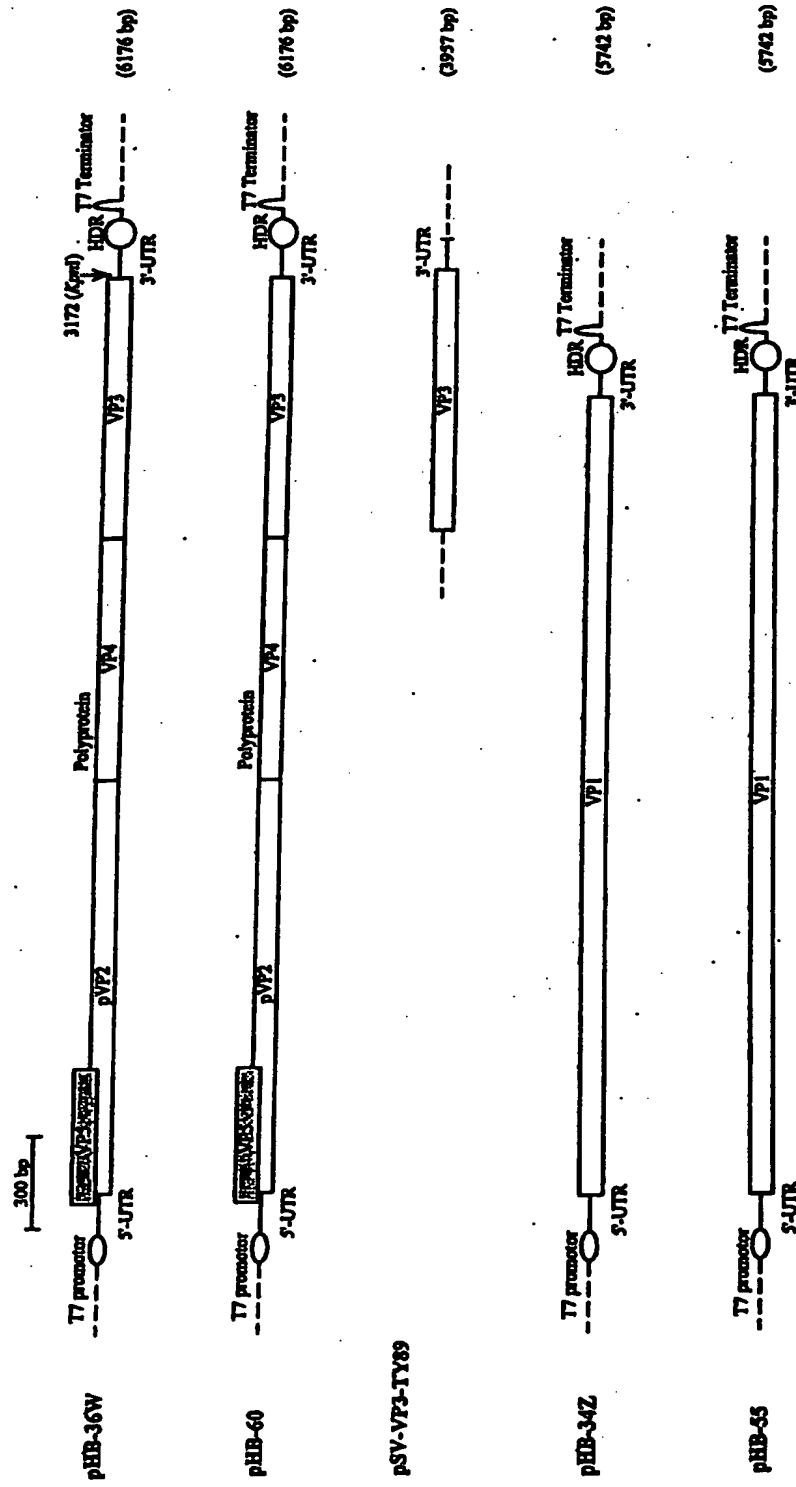
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Fig. 3c IBDV VP5 alignment.

Consensus	MVSRDQTNDR SPD.PARSHP TDCSVHTFES DANKHTGVHS GRNP.EANSQ	50
D6948-VP5E.....R.....	50
CEP94-VP5K.....G.....	50
Consensus	VRDLDLQFDC GGHRVRANCL FFW.FWLANCG CSLHTAEQWE LQVRSDAFDC	100
D6948-VP5F.....	100
CEP94-VP5I.....	100
Consensus	PEPTQQLQLL QASESESSE VIGHT.WWRLC TK.HKKRDL FRKPE	145
D6948-VP5F.....W.....	145
CEP94-VP5S.....R.....	145

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Fig. 4 Schematic representation of the used plasmids



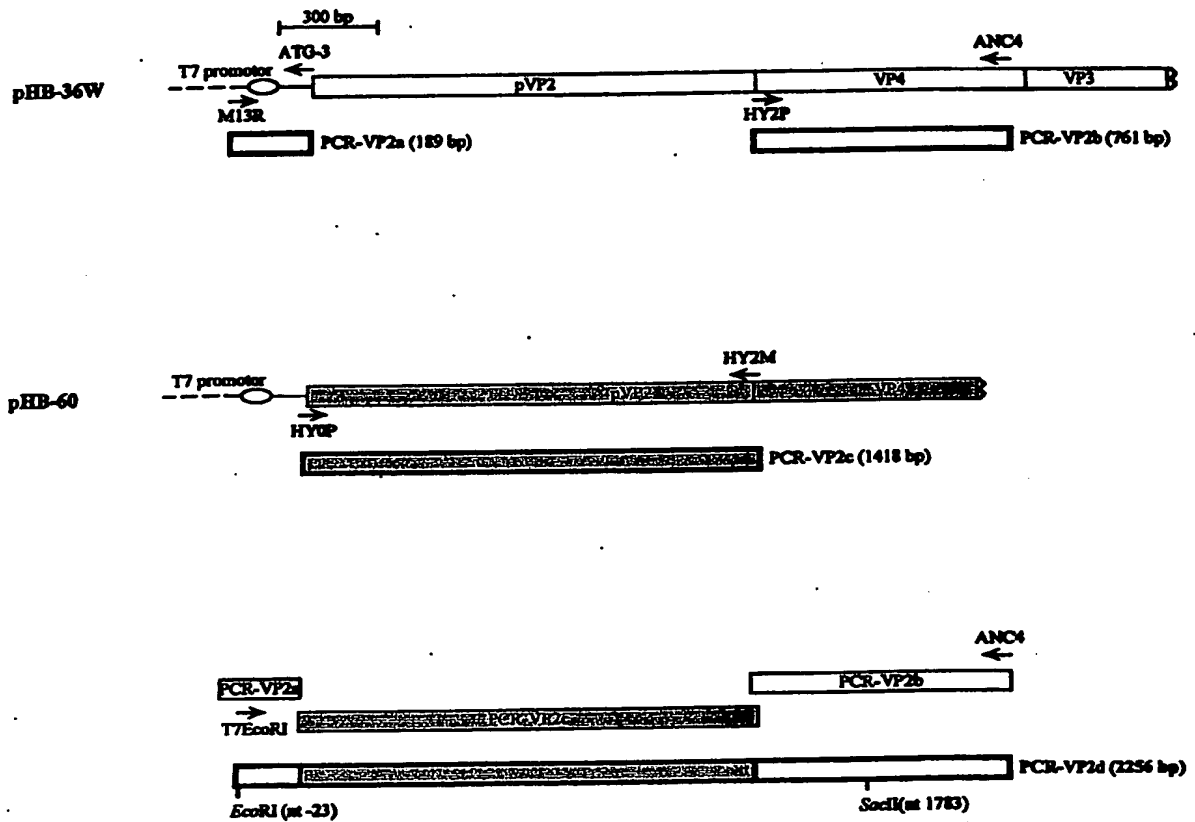
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Fig. 5a

Schematic representation of the construction of PCR fragment PCR-VP2d



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Fig. 5b

Schematic representation of the construction of PCR fragment PCR-VP3c

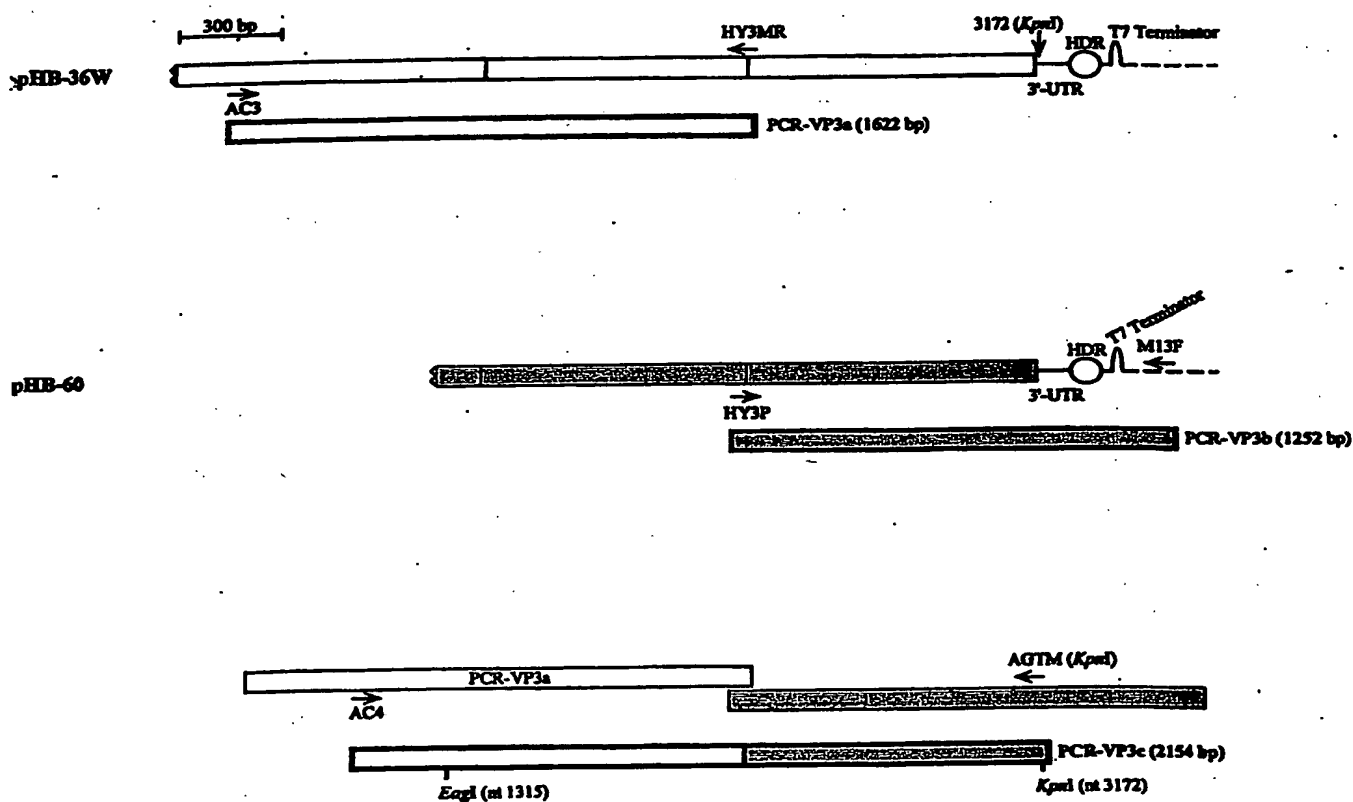
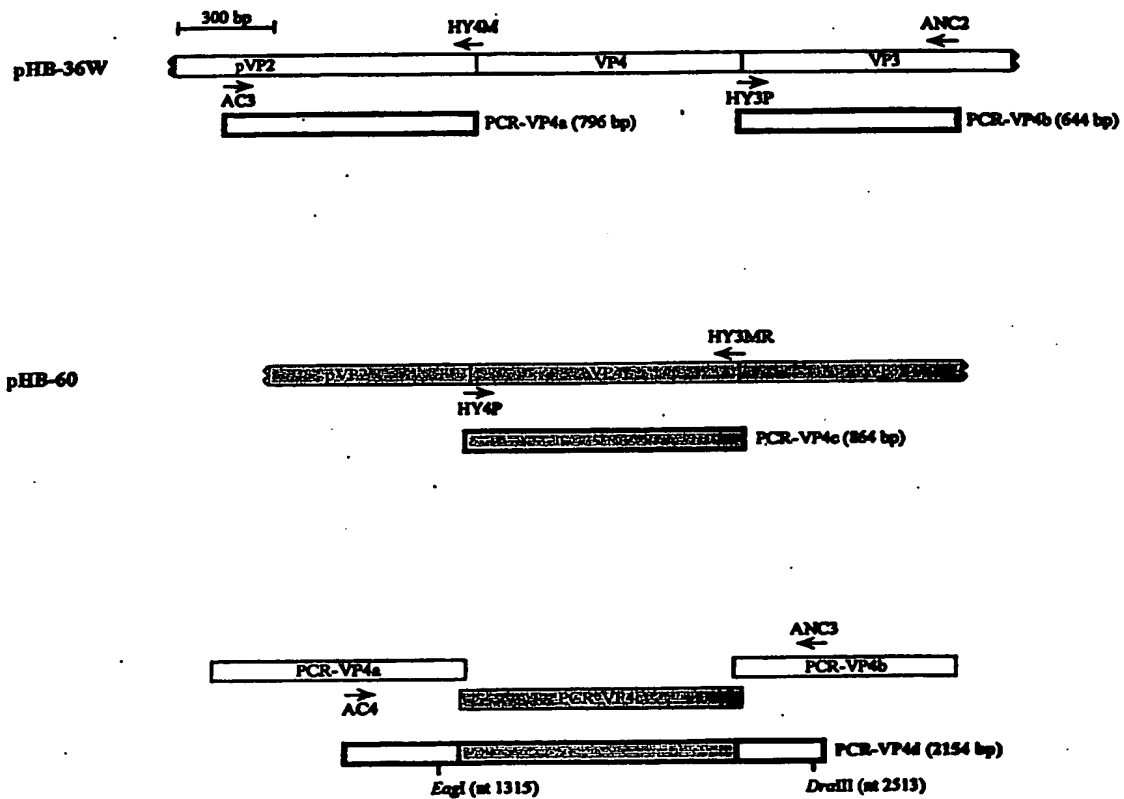


Fig. 5c Schematic representation of the construction of PCR fragment PCR-VP4d



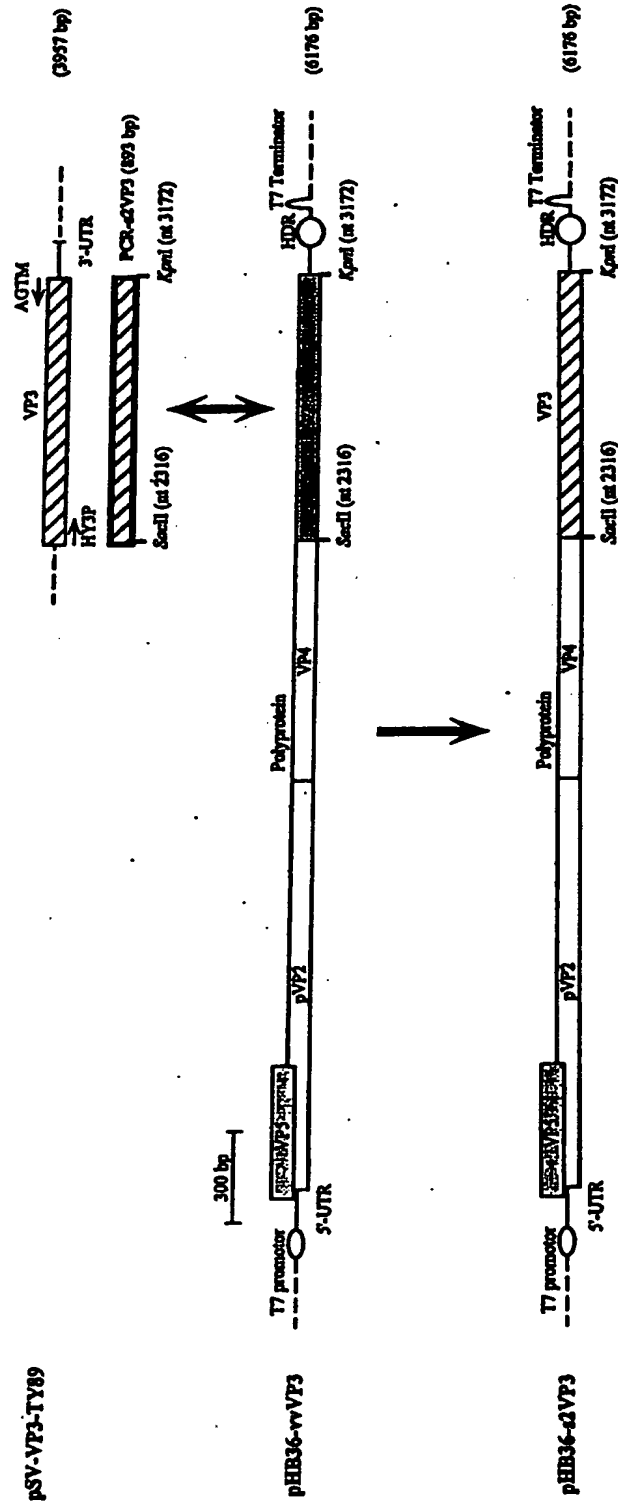
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Fig. 5d Schematic representation of the construction of plasmid pHB36-ΔVP3

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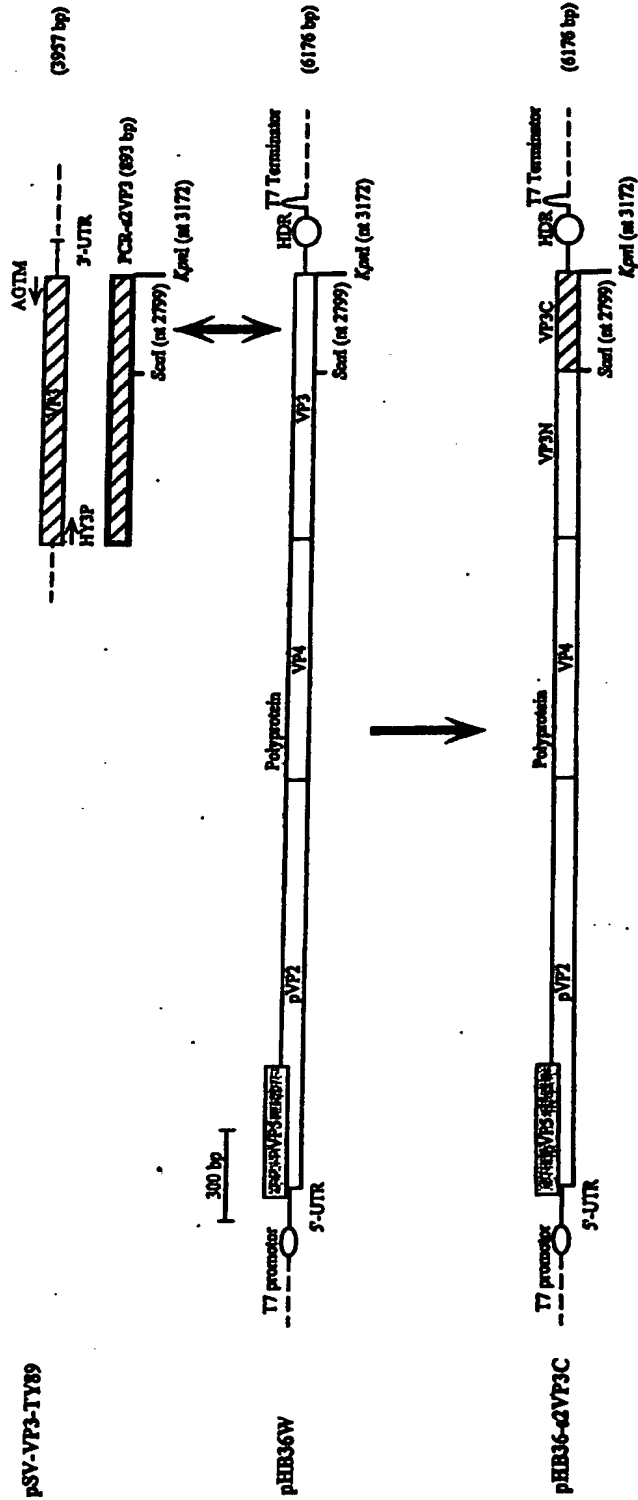
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Fig. 5e

Schematic representation of the construction of plasmid pHB36-ΔVP3C

pSV-VP3-TY89



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Fig. 5f Schematic representation of the construction of plasmid pHB36-ΔVP3N

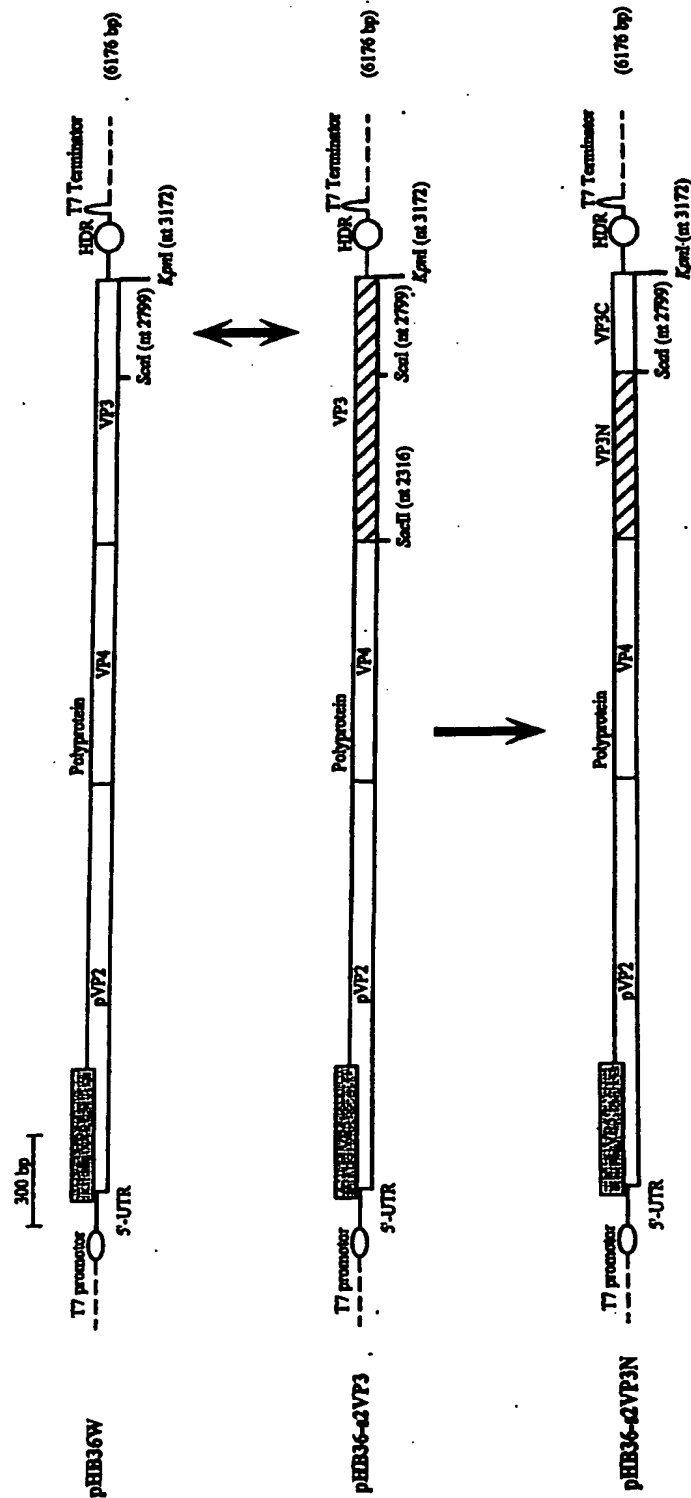
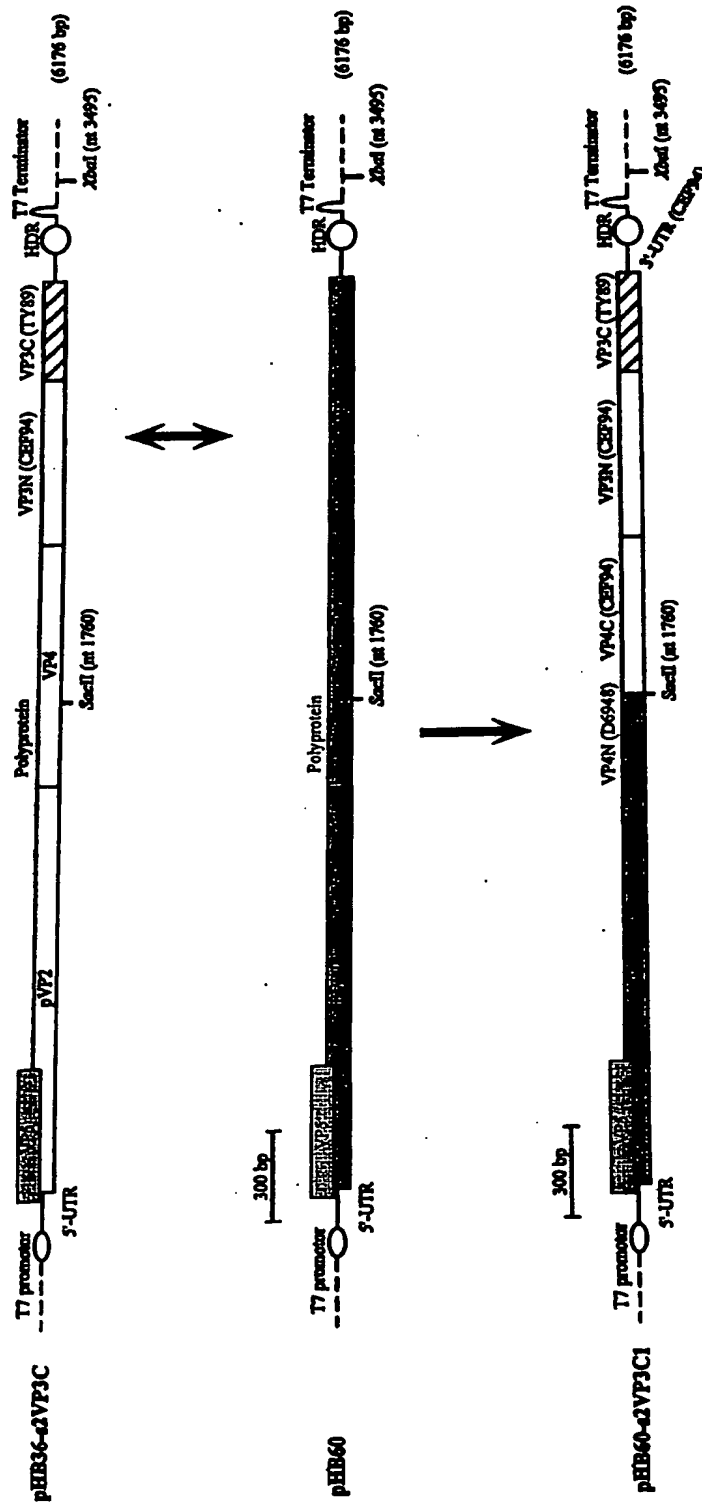


Fig. 5g
Schematic representation of the construction of plasmid pHB60- α VP3C1



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Fig. 6

CEF94-PP TY89-PP	<p> \swarrow SacII 724-FPHNPRD WDRLPYLNL P YLPPNAGROY HLAHAASEFK ETPELESVR AMEAAANVDP LFQSALSVFM WLEENGIVTD 800 724-.....T.....P...L.....D....D....R...Q... ..800 </p>
CEF94-PP TY89-PP	<p> \swarrow SacI MANFALSDPN AHRMRNPLAN APQAGSKSOR AKYGTAGYGV EARGPTPEEA QREKDTTRISK KMETMGIFYA TPENVALNGH 880 K..... ..880 </p>
CEF94-PP TY89-PP	<p> RGPSPGQLKY WONTREIPDP NEDYLDYVHA EKSRLASEEQ ILRAATSIYG APQQAEPPOA FIDEVAKVYE INHGRGPNQE 960 E.....P.....V.....R... ..960 </p>
CEF94-PP TY89-PP	<p> QMKDLLLLTAM EMKERNPRA LPKPKPKPNA PTQRPQRLG RNIRTVEDEE LE 1012 P.....S..... ..1012 </p>

VP4 \longleftrightarrow VP3

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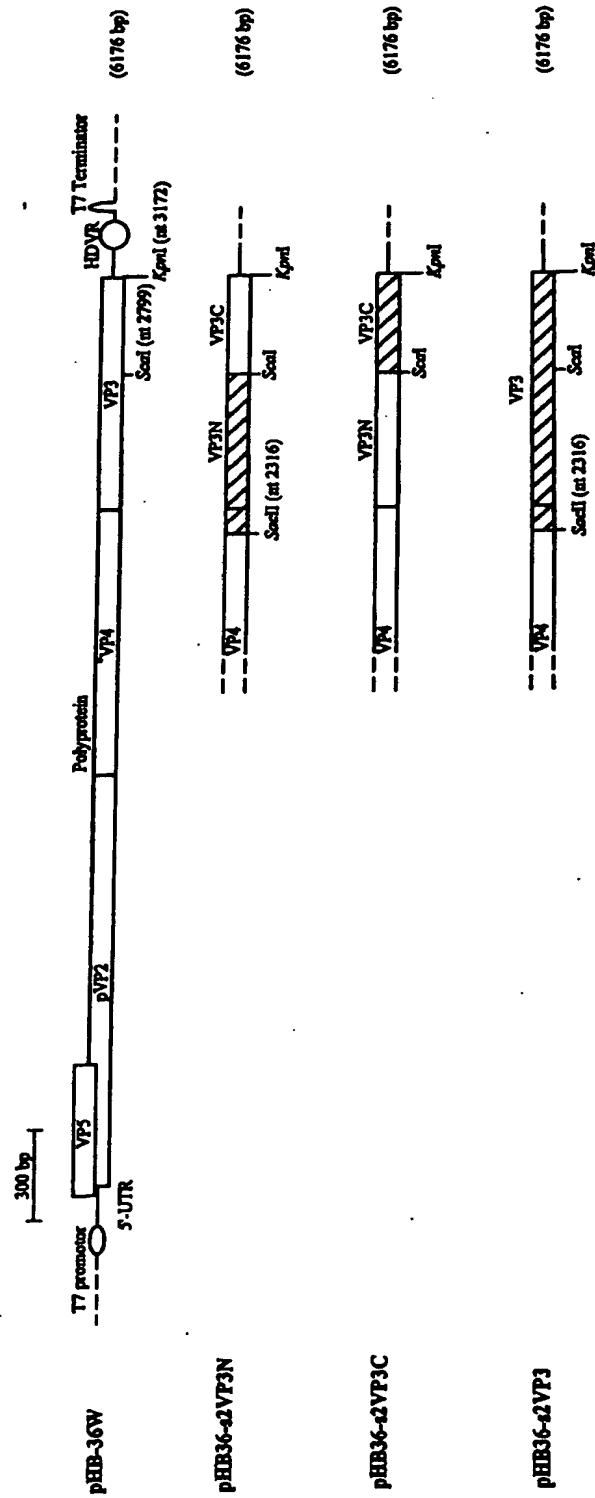


Fig. 7

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Fig. 8C

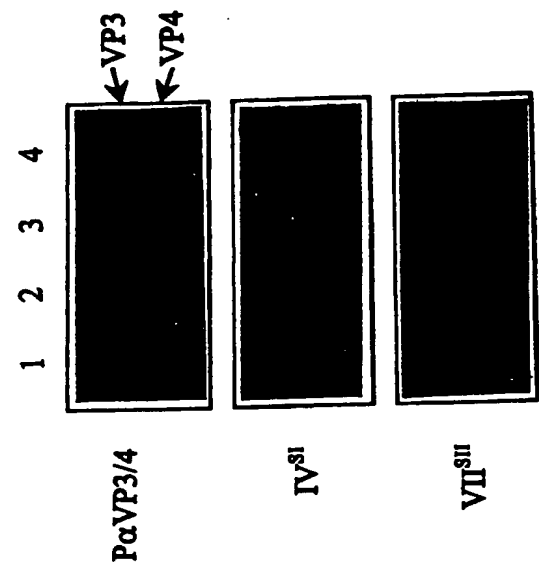


Fig. 8B

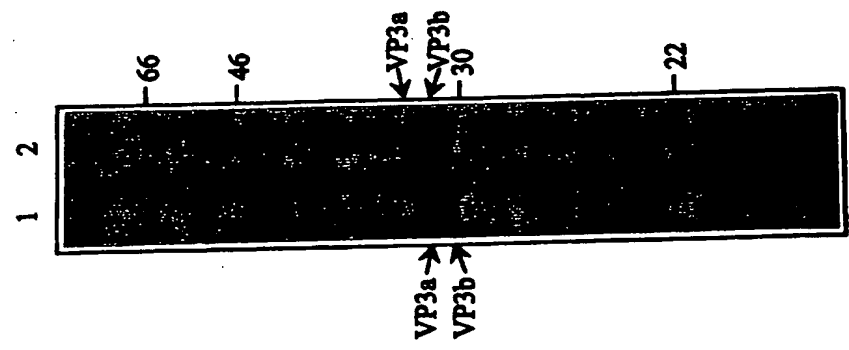
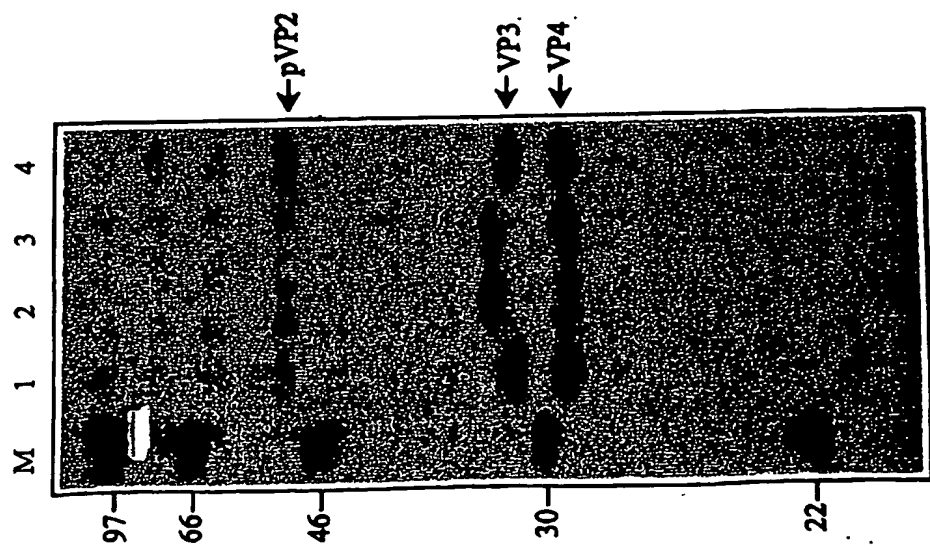


Fig. 8A



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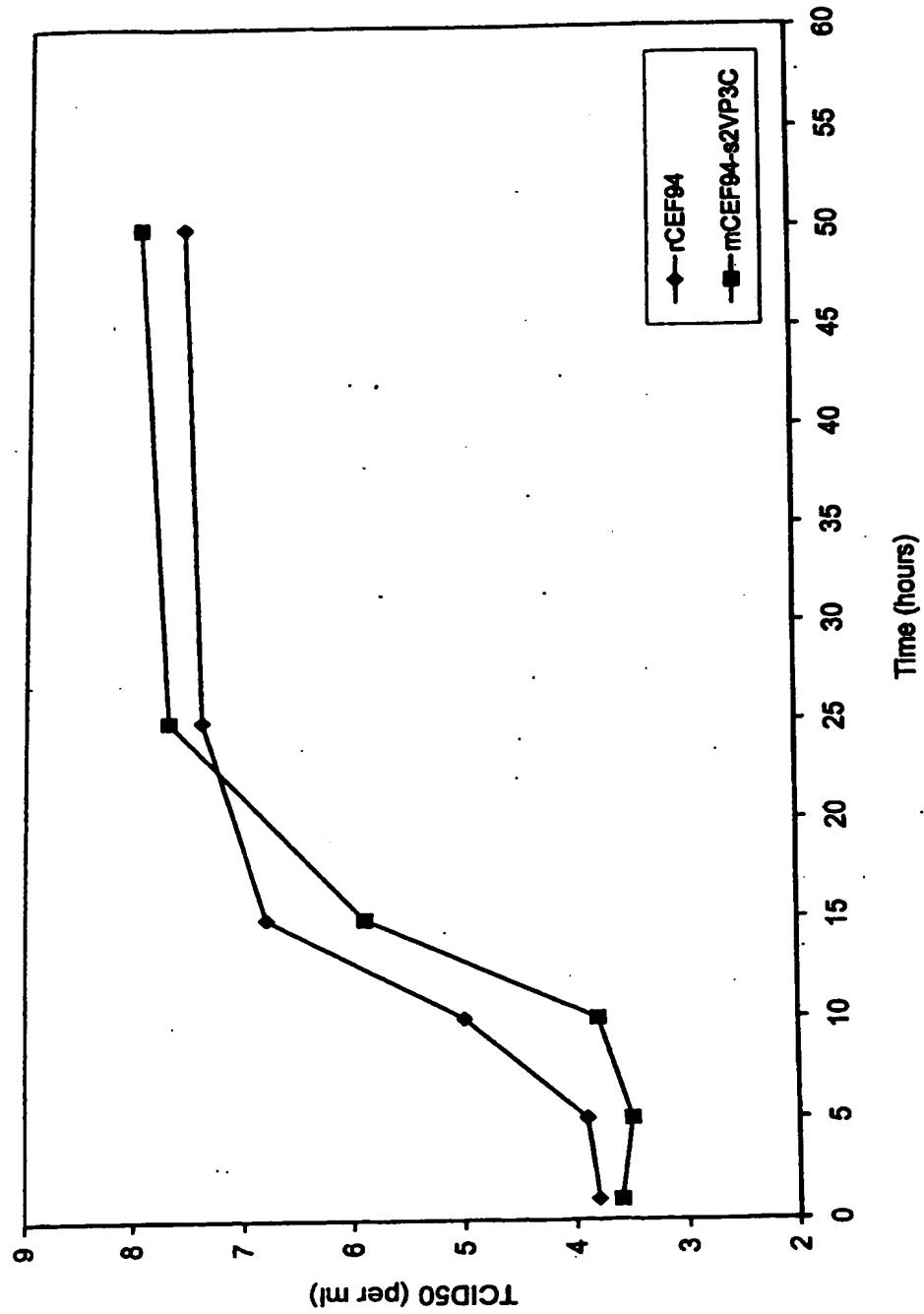


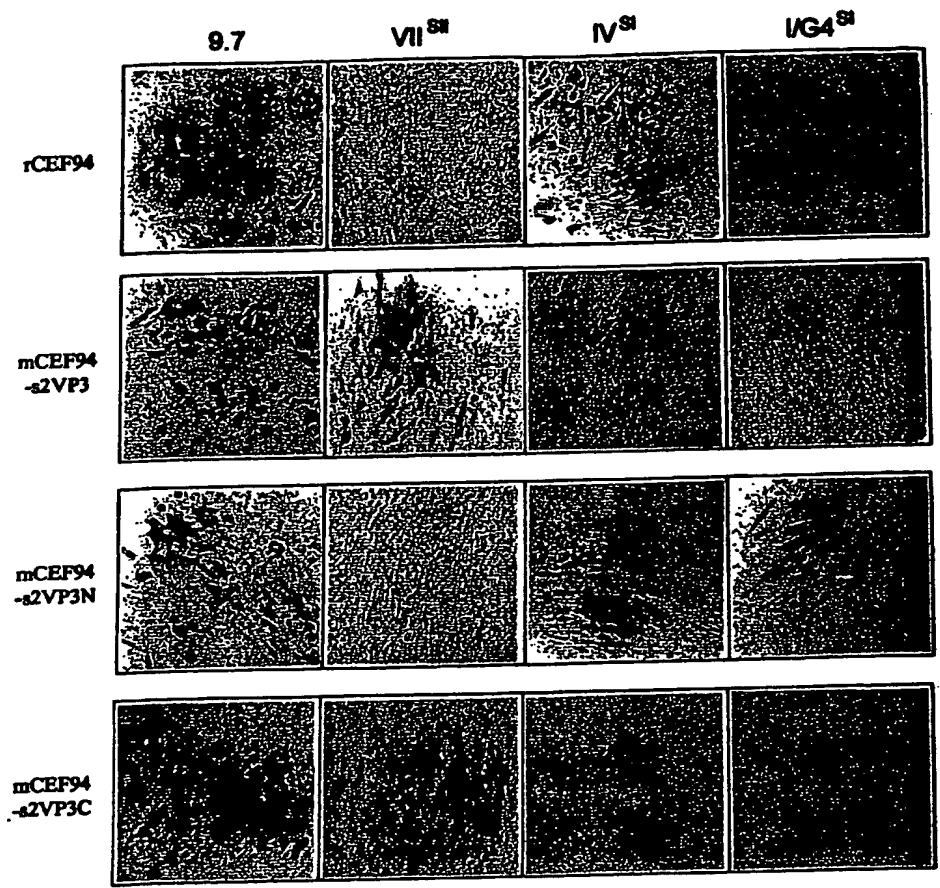
Fig. 9

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Fig. 10



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Schematic representation of plasmids pHB60-s2VP3C1 and pHB60-s2VP3C3

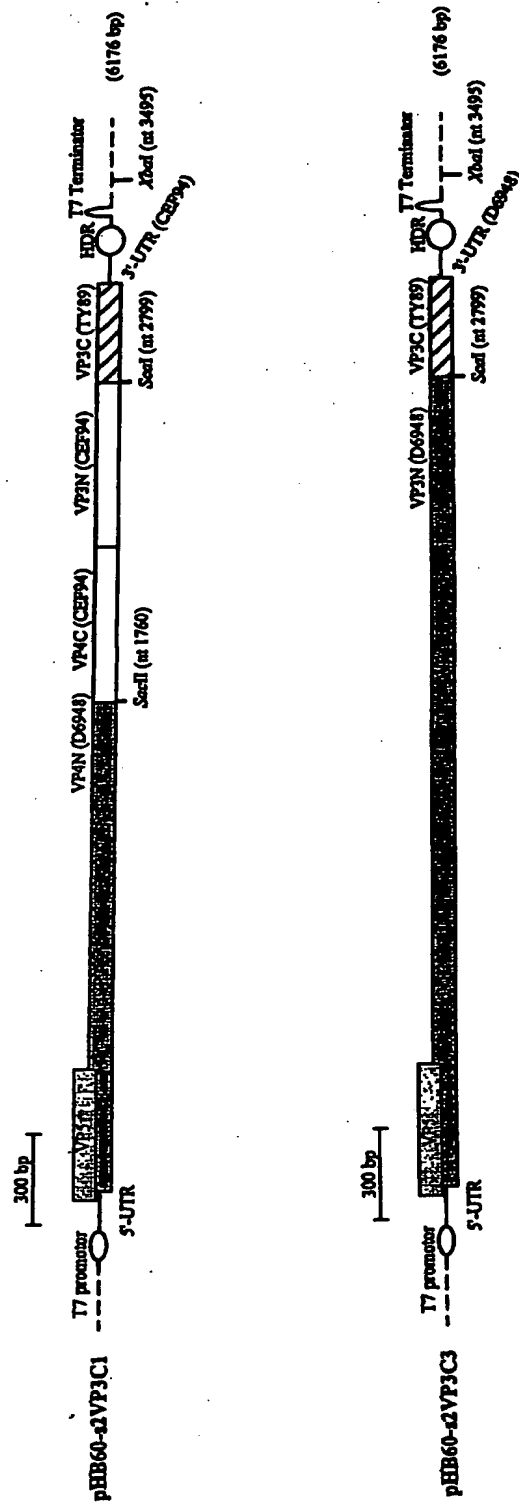


Fig. 11

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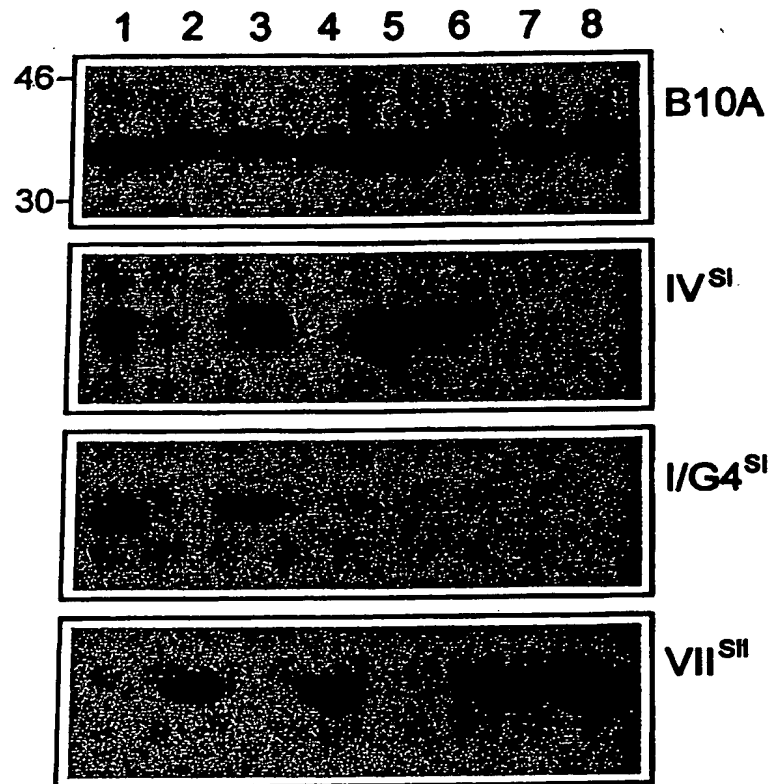
Fig. 12

Fig. 13

VP4 ← VP3
 ↙ SacII
 724-PP FPHNPRD WDRLPYLNL P YLPPNAGRQY HLAWAASEFK ETPELESVR AMEAANVDP LFQSALSVM WLENGIYTD 800
 D6948 724-..... D.....
 TY89-PP 724-..... T..... P..... L..... D..... R..... Q..... 800
 800
 MANFALSDPN AHRMRNFLAN APOAGSKSR AKYGTAGYGV EARGPTPERA QREKDRISK KMETGIYFA TPEWVALNGH 880
 D6948
 TY89-PP K..... 880
 880
 RGPSPGOLKY MONTREIPDP NEDYLDYVEA EKSLASEEQ ILRAATSIYG AFGQAEPPQA FIDEVAKVE INHGRGPNQE 960
 D6948
 TY89-PP E..... P..... V..... R..... 960
 960
 QMKDLLLTAM EMKRNPRRA LPKPKPKPNA PTQPPGRLG RWIRTVSDED LE 1012
 D6948 P..... A..... 1012
 TY89-PP P..... S..... 1012
 1012

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Fig. 14

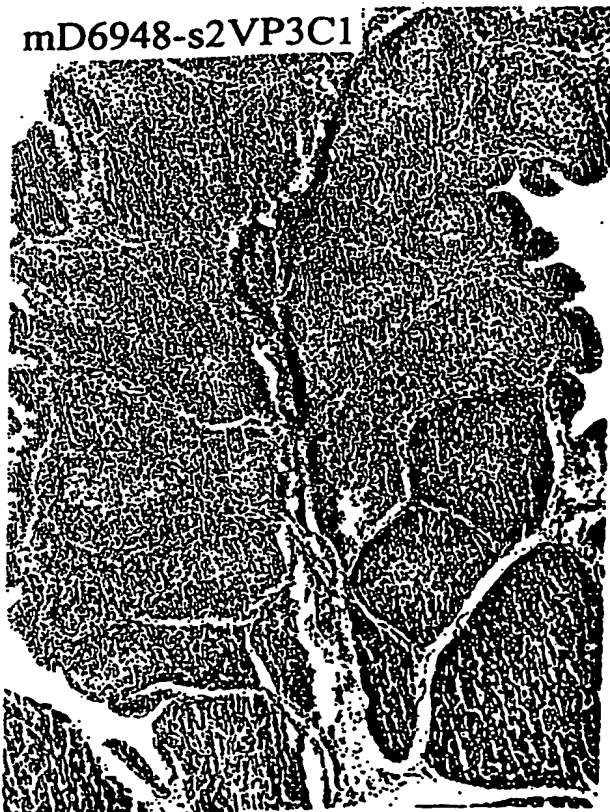
Mock



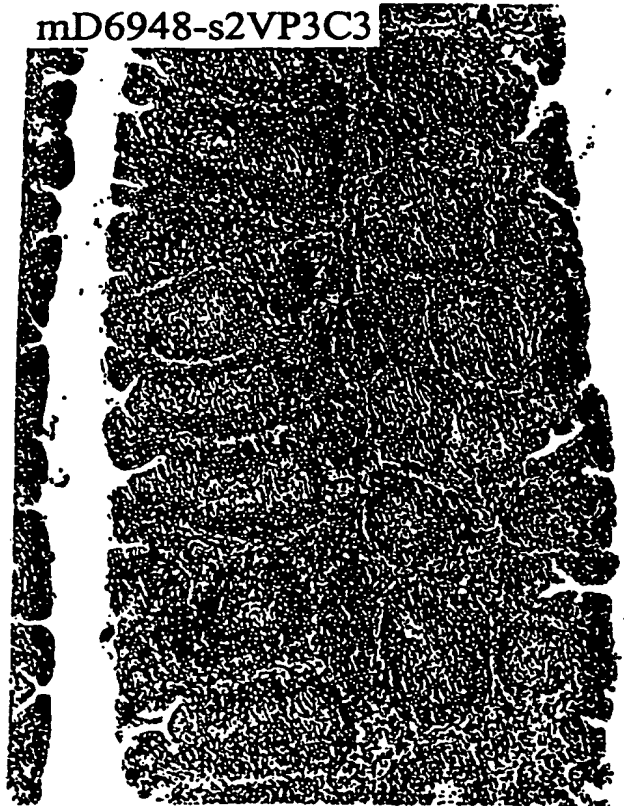
D6948



mD6948-s2VP3C1



mD6948-s2VP3C3



TITLE: MOSAIC INFECTIOUS BURS
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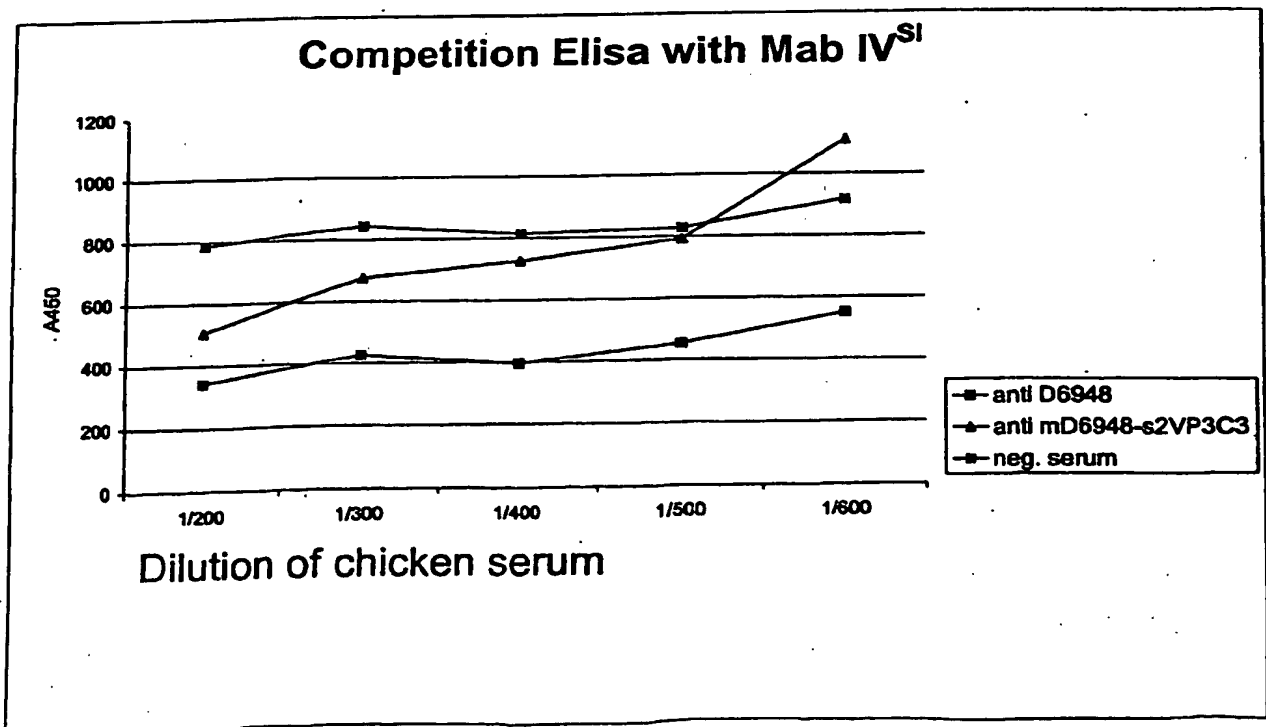
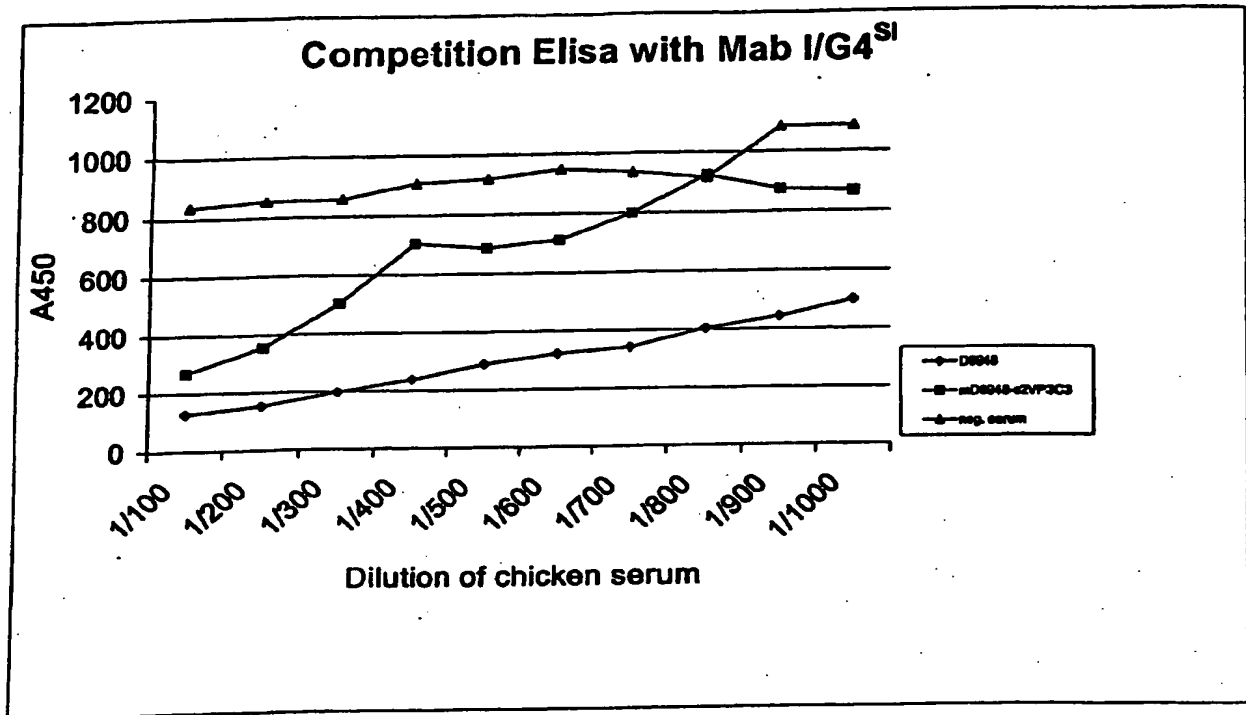
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FIG. 15



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Fig. 16A

D6948-VP5	MLSLMVRDQ	TNDRSDEPA	RSNPTDCSVH	TEPSDANNRT	GVHSGRHPRE	AHSQVRDLDL	QFTCGGHRVR	ANCLF	75
CEF94-VP5	-----	K			G				71
	PWPPWLNCGC	SLHTAEQNEL	QVRSDAPDCP	EPTGQLQLLQ	ASESESHSEV	KHTPWRLCT	KNEHKRRDLP	RKPE	149
	I			S		R			145

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Fig. 16B

D6948-PP MTNLQDQTOQ IVTFIRSLM PTTOPASIPD DTLEKHTLRS ETSTYNLTVG DTGSLIVFF PGFPGSIVGA HYTLQ 75
 CEF94-PP SNGNYKFDQM LLTAQNLPAS YNYCRLVRSR LTVRSSTLPG GVVYALNGTIN AVTFQGSLSL LTDVSINGLM SATAN 150
 INDKIGNVLV QEGVTVLSP TSYDLGYVRL GDPIPAIGLD PKWVATCDSS DRPRVYTITA ADDYQFSSQY QAGGV 225
 TITLFSANID AITSLSIGGE LVFQTSVQGL ILGATYILIG FDGTAVITRA VAADNGLTAG TDNLMPFNIV IPTSE 300
 ITQPIITSIKL EIVTSKSGGQ AGDOMSWSAS GSLAVTINGG NYPCALRPVT LVAYERVATO SVVTVAGVSN FELIP 375
 NPFLAKNLVT EYGRFDPQAM NYTKLILSER DRLGINKTWP TREYTDREY FMEVADINSP LKLAGAFGEK DIIRA 450
 LRRJAVPVVS TLEPPAAPLA HAIGEGVDYL LGDEAORASG TARRASGKAR AASGRITOLT LAADKGYEVV ANLEQ 525
 YRONVVVDGI LASPGILGGA HNLDCLVREG ATLEPVVITT VEDANTPKAL NKKMEAVIEG VRELOPPSO RGSFI 600
 RTLSGHRVYG YAPDGVLEP LRGDYTVVPI DDVMDDBIML SKDPIPIVG NSGNLAIAYM DVEPKVPIH VAMTG 675
 ALNAYGBIEN VSRSTKLAT AHRIGLKLKAG PGAFDVNTGS NWATFLKRP ENPRDWDRLP YMLPYLPPN AGROY 750
 DLAMAASEFK ETPELESVR AMEAAANVDP LFQSALSVM WLENGIYTD MANFALSDEPN AHRMRNFLAN APQAG 825
 SKSQRAKYGT AGYGVREARCP TPEAQREKD TRISKMETM GIYFATPEWV ALNGHROPSP GOLKIYQWNT RIPP 900
 NEDYLDYVHA EKSRLASEQ ILRAATSIYG APQAEPPQA FIDEVAKVE INHGRCPQOE QMKDILLTAM EMKHR 975
 NRRAPPKPK PKPNAPTQRP PGLGRWIRA VSEDELE 1012
 L T

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D6948-VP1
CBP94-VP1

MSDVNSPQA	RSKISAAFGI	KPTAQDVBE	LLIPKVVYPP	EDPLASPSRL	AKFLRENGYK	ILQPRSLPEN	BEYET	75
I	T				V			
DQILPDIAWM	QJIEGAVLKP	TLSLPIGDQE	YPPKYYPTHR	PSKEKPNAYP	PDIALLIKQMI	YLFLOVPEAT	DNLKD	150
					N	EQ		
EVTLTQWIR	DKVSGGTYM	QOATRLVAMK	EVATGRPNPK	DPLKLGTYFE	SIAQLLDITL	PVGPPQEDDK	PWVPL	225
TRVPSRMLVL	TGDVDGEFEV	EDYLPKINLK	SSSGLPYVGR	TKGETIGEMI	AISNQFLREL	SALLKQAGT	KGSNK	300
	D				T			
KKLLSMLSDY	WYLSGOLLFP	KAERYDKSTM	LTKTRNINSA	PSPTHLMISM	ITWPMNSNP	NNVLNIEGCP	SLYKP	375
NPFRGGLNRI	VEWIMAPDEP	KALVYADNIY	IVHSNTWYSI	DLEKGEANCT	ROHMQAAMY	ILTRGWSDNQ	DPMPN	450
	L	E						
QTWATFAMNI	APALVVDSSC	LIMNLQIKTY	QGSGGNAATP	INNHLSTLY	LQDNLMLKQP	SPDSBEFKSI	EDKLG	525
					R	R		
INFKERSID	DIRGKLRQLV	PLAQPOYLSC	GVEPEQSPPT	VELDLLGWSA	TYSKDLGIYV	PVLDKERLFC	SAAYP	600
	L		S					
KGVENKSLKS	KVGIBQAYKV	VRYEALRLVG	GMNYPLANKA	CKNNASAAAR	HLEAKGFPLO	EFLAENSELS	EPQEA	675
				G				
PEGFNIKLTV	TPESLAEALNR	PVPPKPPNVN	RPVNTGOLKA	VSNALKTGRY	RNEAGLSGLV	LLATABRLQ	DAVKA	750
	S	X						
KABAEKLHKS	KPDDPDADWF	ERSETLSDLL	EKADIASKVA	HSAUVETSDA	LEAVQSTSVY	TPKYPEVKNP	QTASN	825
PVVGLHLPAP	RATGVQAALL	GAGTSRPMGM	EAPTRSKNAV	KMAKRRQROK	ESRQ--			879
					QP			881

TITLE: MOSAIC INFECTIOUS BURSA
DISEASE VIRUS VACCINES

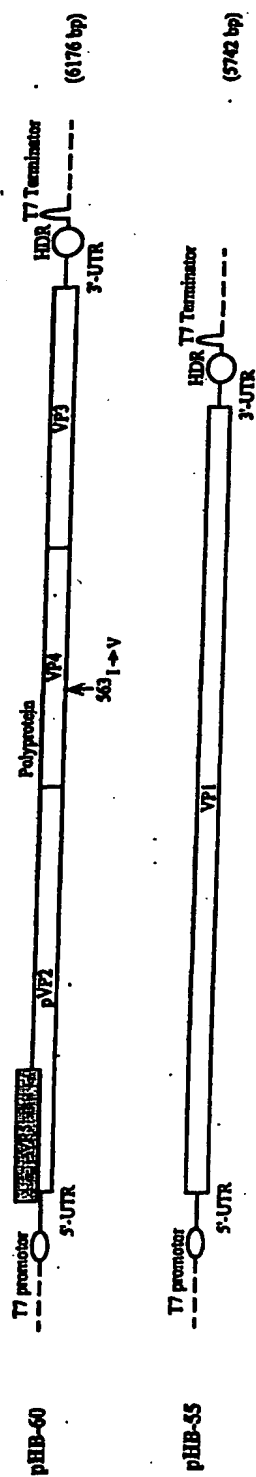
Inventor: Boot et al.

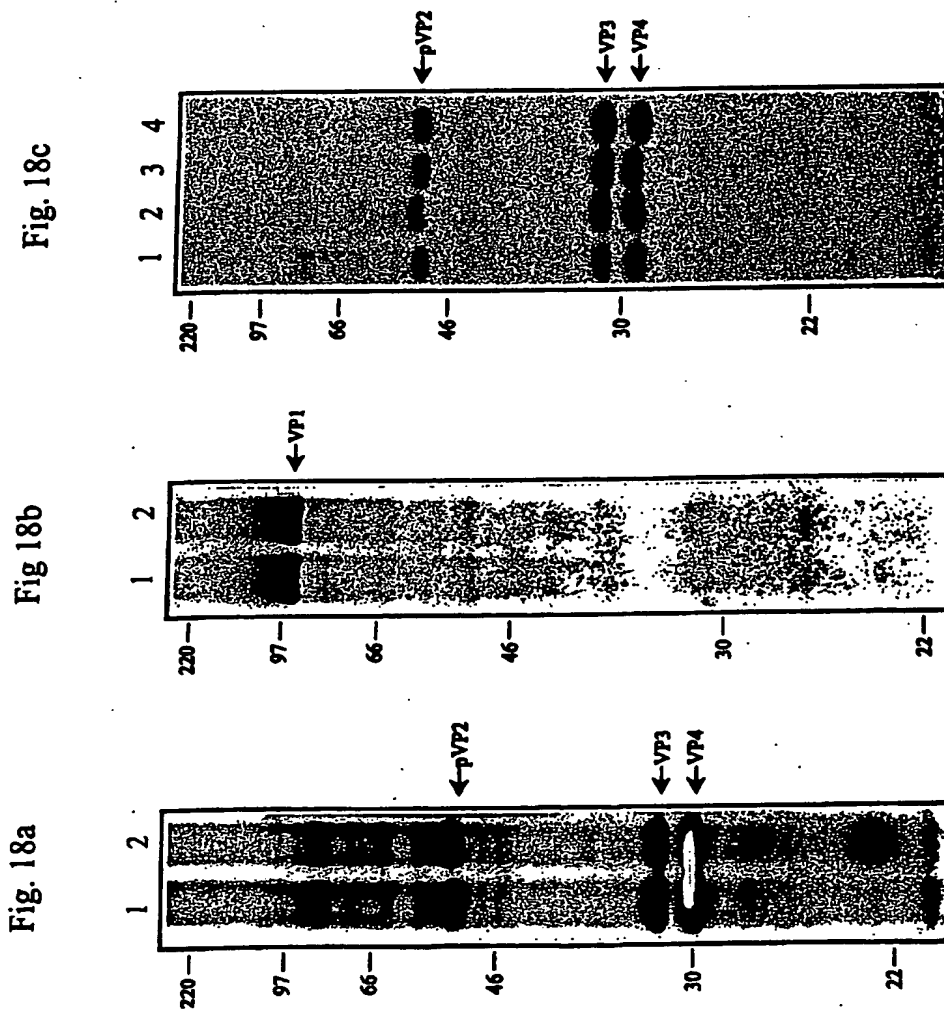
Serial No.: 10/046,671

Docket No.: 2183-5238US

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Fig. 17

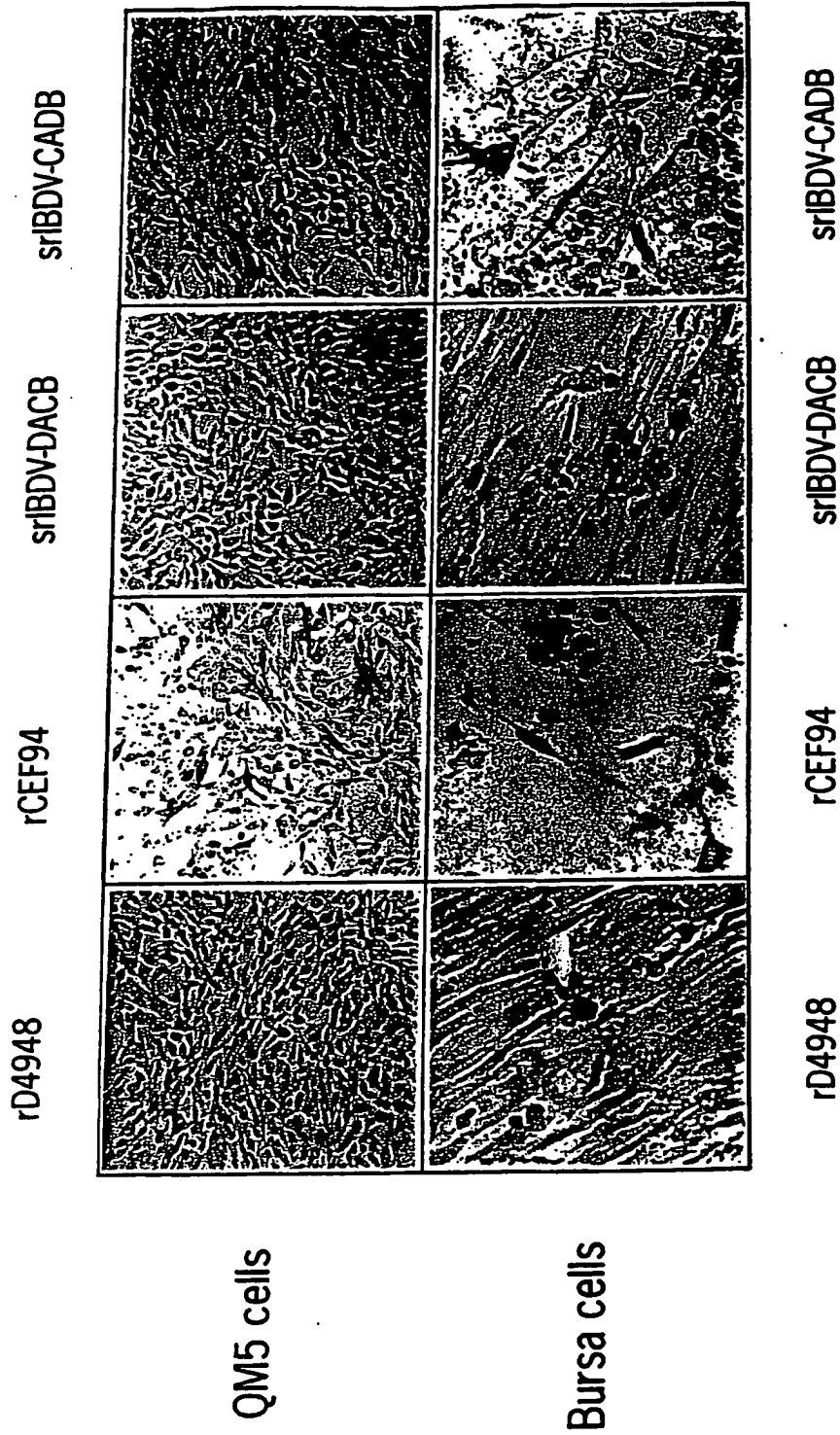




TITLE: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINESInventor: Boot et al.
Serial No.: 10/046,671
Docket No.: 2183-5238US

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Fig. 19



TITLE: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINES
Inventor: Boot et al.
Serial No.: 10/046,671
Docket No.: 2183-5238US

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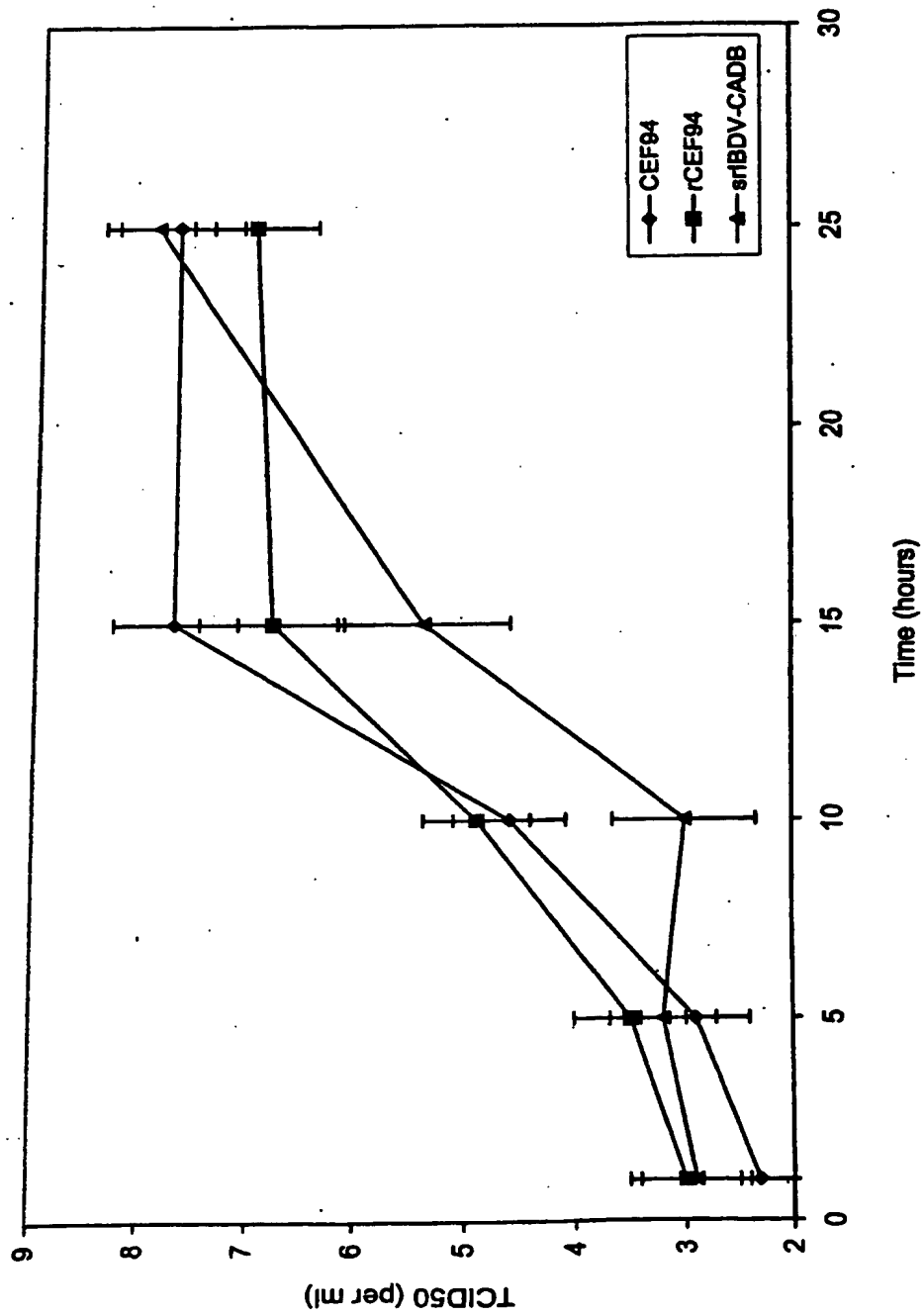
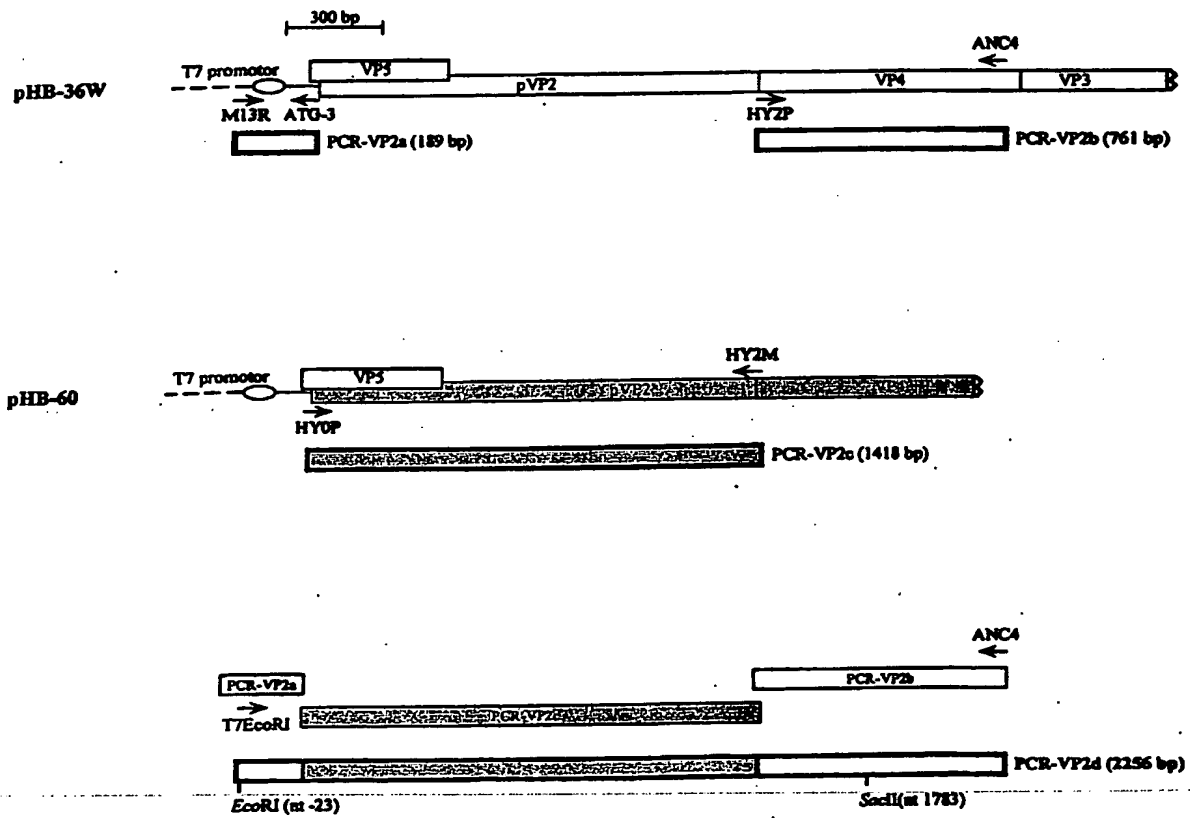


Fig. 20

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Fig. 21



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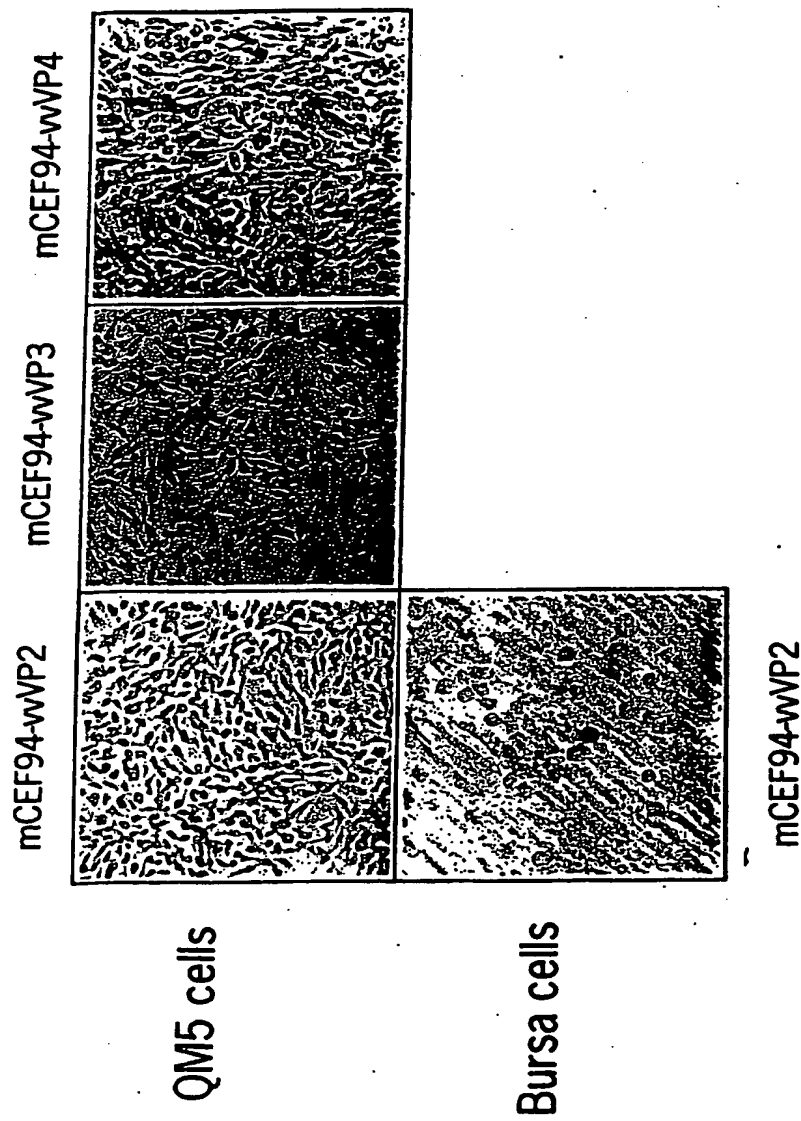


Fig. 22